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OM nucleic - nucleic search, using sw model
Run on: March 4, 2005, 09:25:48 ; Search time 6803 Seconds
(without alignments)
3183.813 Million cell updates/sec

Title: US-09-851-138C-51
Perfect score: 447
Sequence: 1 gacgaataatttcgaac.....aggactgcaactgttccatc 447

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.tv.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	445.8	99.7	447	6 A50396	A50396 Sequence 51
2	445.8	99.7	447	6 ARI27536	ARI27536 Sequence
3	445.8	99.7	447	14 HPCJ0049A5	L39317 Hepatitis C
4	393	87.9	1584	14 HPCJ0049A5	D49749 Hepatitis C
5	393	87.9	1584	14 HPCJ0055A6	D49750 Hepatitis C
6	393	87.9	1584	14 HPCJ0070A8	D49752 Hepatitis C
7	393	87.9	9450	14 HPCJ0049E1	D63821 Hepatitis C
8	389.8	87.2	1584	14 HPCJ0030A3	D49747 Hepatitis C
9	388.2	86.8	1584	14 HPCJ0072A9	D49753 Hepatitis C
10	322.8	72.2	411	14 HPCCP3	D30046 Hepatitis C
11	255.8	57.2	1505	14 HPCNE125C	D16614 Hepatitis C
12	252.2	56.4	1505	14 HPCNE27A1	D16620 Hepatitis C
13	244.4	54.7	867	14 HPCNCV048	D16736 Hepatitis C
14	241.2	54.0	1504	14 HPCNCV137E	D16618 Hepatitis C
15	239.4	53.6	447	14 HPCCOREE1S	L39298 Hepatitis C
16	238.2	53.3	1504	14 HPCNE145G	D16612 Hepatitis C
17	236.6	52.9	1504	14 HPCNE048A	D16612 Hepatitis C
18	236.4	52.9	867	14 HPCNCV049	D16737 Hepatitis C
19	236.2	52.8	541	6 A40613	A40613 Sequence 13

20	236.2	52.8	541	6 A40617	A40617 Sequence 17
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22	236.2	52.8	541	6 BD172132	BD172132 New seque
23	236.2	52.8	541	6 AX031591	AX031591 Sequence
24	236.2	52.8	541	6 AX031595	AX031595 Sequence
25	236.2	52.8	541	6 AX031861	AX031861 Sequence
26	236.2	52.8	541	6 AX031865	AX031865 Sequence
27	236.2	52.8	541	6 AX032131	AX032131 Sequence
28	236.2	52.8	541	6 AX032135	AX032135 Sequence
29	236.2	52.8	541	14 HPCCOREEH	D14603 Hepatitis C
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31	234.6	52.5	541	6 A40619	BD172133 New seque
32	234.6	52.5	541	6 BD172133	BD172133 Sequence
33	234.6	52.5	541	6 AX031597	AX031597 Sequence
34	234.6	52.5	541	6 AX031867	AX031867 Sequence
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37	234.6	52.5	9456	14 HPCEGS	D17763 Hepatitis C
38	233	52.1	541	6 A40615	A40615 Sequence 15
39	233	52.1	541	6 A40621	A40621 Sequence 21
40	233	52.1	541	6 A40625	A40625 Sequence 25
41	233	52.1	541	6 A40627	A40627 Sequence 27
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ALIGNMENTS

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

A50396
Sequence 51 from Patent WO9613590.
A50396
A50396.1 GI:2303407
unidentified
unclassified.
1 (bases 1 to 447)
Maertens, G. and Stuyver, L.
NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS
PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC AGENTS
Patent: WO 9613590-A 51 09-MAY-1996;
INNOGENETICS NV (BE)
Other publication AU 3844095 960523.
Location/Qualifiers
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PAT 07-MAR-1997

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Qy	61	GTTTGTCTTCATGCTTGTACACCCAGCCGCGGCTGGAGTACCGTAATGCCTCCGA	120				
Db	61	GTTTGTCTTCATGCTTGTACACCCAGCCGCGGCTGGAGTACCGTAATGCCTCCGA	120				
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Qy	181	ATCTCCCACTTACCTGGCTGTGTCCTCGCTGCGCAATACATCAAGATGCTCG	240				
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QY 421 ACTGTCAGAGTGCAGTGTTCATC 447
Db 421 ACTGTCAGAGTGCAGTGTTCATC 447

RESULT 2
LOCUS AR127536
DEFINITION Sequence 51 from patent US 6180768.
ACCESSION AR127536
VERSION AR127536.1 GI:14114131
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 447)
AUTHORS Maertens,G. and Stuyver,L.
TITLE Sequences of hepatitis C virus genotypes and their use as prophylactic, therapeutic and diagnostic agents
JOURNAL Patent: US 6180768-A 51 30-JAN-2001;
FEATURES
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    Best Local Similarity 100.0%; Pred. No. 9.6e-109;
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QY 421 ACTGTCAGAGTGCAGTGTTCATC 447
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Db 421 ACTGTCAGAGTGCAGTGTTCATC 447

RESULT 3
LOCUS HPCCORREAL
DEFINITION Hepatitis C virus type 3 clone NL96 precursor protein gene, partial cds
ACCESSION L39317
VERSION L39317.1 GI:845497
KEYWORDS
SOURCE Hepatitis C virus type 3
ORGANISM Hepatitis C virus type 3
REFERENCE 1 (bases 1 to 447)
AUTHORS van Doorn,L.J., Kleter,B., Stuyver,L., Maertens,G., Brouwer,H., Schalm,S., Heijtkink,R. and Quint,W.
TITLE Analysis of hepatitis C virus genotypes by a line probe assay and correlation with antibody profiles
JOURNAL J. Hepatol. 21 (1), 122-129 (1994)
MEDLINE 95052487
PUBMED 7525693
REFERENCE 2 (bases 1 to 447)
AUTHORS van Doorn,L.J., Kleter,G.E., Stuyver,L., Maertens,G., Brouwer,J.T., Schalm,S.W., Heijtkink,R.A. and Quint,W.G.
TITLE Sequence analysis of hepatitis C virus genotypes 1 to 5 reveals multiple novel subtypes in the Benelux countries
JOURNAL J. Gen. Virol. 76 (Pt 7), 1871-1876 (1995)
MEDLINE 97201609
PUBMED 9049395
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Qy 421 ACTGTCCAGGACTGCACTGTTCCATC 447
Db 421 ACTGTCCAGGACTGCACTGTTCCATC 447

RESULT 4
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LOCUS      Hepatitis C virus isolate JK049 gene for core, env, and part of
DEFINITION      E2/NS1, partial cds.
ACCESSION      D49749
VERSION      GI:1197110
KEYWORDS      core, env, and part of E2/NS1.
SOURCE      Hepatitis C virus
ORGANISM      Hepatitis C virus
               Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
               Hepacivirus.
REFERENCE      1 (sites)
AUTHORS      Tokita,H., Okamoto,H., Iizuka,H., Kishimoto,J., Teuda,F.,
               Lesmana,L.A., Miyakawa,Y. and Mayumi,M.
TITLE      Hepatitis C virus variants from Jakarta, Indonesia classifiable
               into novel genotypes in the second (2e and 2f), tenth (10a) and
               eleventh (11a) genetic groups
JOURNAL      J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
MEDLINE      96226020
PUBMED      8627233
REFERENCE      2 (bases 1 to 1584)
AUTHORS      Okamoto,H.
JOURNAL      Unpublished
REFERENCE      3 (bases 1 to 1584)
AUTHORS      Okamoto,H.
TITLE      Direct Submission
JOURNAL      Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
               Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
               329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
               Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
               Location/Qualifiers
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ORIGIN
Query Match      87.9%; Score 393; DB 14; Length 1584;
Best Local Similarity 91.9%; Pred. No. 1.5e-94;
Matches 411; Conservative 3; Mismatches 33; Indels 0; Gaps 0;
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Db 817 GAGCGAATTAATTTCCGCAACAGGGAATTTACCTGGTGTGCTCTTCTATCTCTCTTCG 876
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Qy 421 ACTGTCCAGGACTGCACTGTTCCATC 447
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RESULT 5
HPCJK055A6      1584 bp      RNA      linear      VRL 10-FEB-1999
LOCUS      Hepatitis C virus isolate JK055 gene for core, env, and part of
DEFINITION      E2/NS1, partial cds.
ACCESSION      D49750
VERSION      GI:1197114
KEYWORDS      core, env, and part of E2/NS1.
SOURCE      Hepatitis C virus
ORGANISM      Hepatitis C virus
               Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
               Hepacivirus.
REFERENCE      1 (sites)
AUTHORS      Tokita,H., Okamoto,H., Iizuka,H., Kishimoto,J., Teuda,F.,
               Lesmana,L.A., Miyakawa,Y. and Mayumi,M.
TITLE      Hepatitis C virus variants from Jakarta, Indonesia classifiable
               into novel genotypes in the second (2e and 2f), tenth (10a) and
               eleventh (11a) genetic groups
JOURNAL      J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
MEDLINE      96226020
PUBMED      8627233
REFERENCE      2 (bases 1 to 1584)
AUTHORS      Okamoto,H.
JOURNAL      Unpublished
REFERENCE      3 (bases 1 to 1584)
AUTHORS      Okamoto,H.
TITLE      Direct Submission
JOURNAL      Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
               Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
               329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
               Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
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ORIGIN
Query Match      87.9%; Score 393; DB 14; Length 1584;
Best Local Similarity 91.9%; Pred. No. 1.5e-94;
Matches 411; Conservative 3; Mismatches 33; Indels 0; Gaps 0;
QY 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTGTCTTTCTCTATCTTCTCTG 60
DB |||||
QY 61 GCTTTGTTCTCATGCTTCTTACACCCACAGCCGGCTGGAGTACCGTAATGCCCTCCGGA 120
DB |||||
QY 817 GCTTTGCTTTCATGCTTGTCTTACACCCACAGCCGGCTGGAGTACCGTAATGCCCTCCGGA 936
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QY 421 ACTGTCCAGGACTGCACTGTTCATC 447
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QY 1237 ACTGTCCAGGACTGCACTGTTCATC 1263
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LOCUS
DEFINITION Hepatitis C virus isolate JK070 RNA linear VRL 10-FEB-1999
E2/NS1, partial cds.
ACCESSION D49752
VERSION D49752.1
KEYWORDS core, env, and part of E2/NS1.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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1 (sites)
Tokita,H., Okamoto,H., Iizuka,H., Kishimoto,J., Tauda,F.,
Legmana,L.A., Miyakawa,Y. and Mayumi,M.
Hepatitis C virus variants from Jakarta, Indonesia classifiable
into novel genotypes in the second (2e and 2f), tenth (10a) and
eleventh (11a) genetic groups
J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
96226020
8627233
2 (bases 1 to 1584)
Okamoto,H.
Unpublished
JOURNAL
AUTHORS Okamoto,H.
REFERENCE
3 (bases 1 to 1584)
Direct Submission
Okamoto,H.
Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
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Db 1237 ACTGTTTCAGGAGTGCACAACTGTTTCGATC 1263

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DEFINITION Hepatitis C virus isolate.JK049 genomic RNA for polyprotein,
complete genome.
ACCESSION D63821
VERSION D63821.1 GI:1183032
KEYWORDS polyprotein.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (sites)
AUTHORS Tokita.H., Okamoto,H., Iizuka.H., Kishimoto.J., Tada.F.,
Lesmana,L.A., Miyakawa.Y. and Mayumi.M.
TITLE Hepatitis C virus variants from Jakarta, Indonesia classifiable
into novel genotypes in the second (2e and 2f), tenth (10a) and
eleventh (11a) genetic groups
JOURNAL J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
MEDLINE 96226020
PUBMED 8627233
REFERENCE 2 (bases 1 to 9450)
AUTHORS Okamoto,H.
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 9450)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1995) Hiroaki Okamoto, Jichi Medical School,
Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
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Best Local Similarity 91.9%; Pred. No. 1.7e-94;
Matches 411; Conservative 3; Mismatches 33; Indels 0; Gaps 0;
Qy 1 GACGGAATTAATTTTCGCAACAGGGGAATTTTACCTGGTGTCTCTTTCTATCTCTCTCTG 60
Db 817 GACGGAATCAATTTTCGCAACAGGGGAATTTTACCTGGTGTCTCTTTCTATCTCTCTCTG 876
Qy 61 GCTTTGTTCTCATGCTTGTACACCCACAGCGGGCTGGAGTACCGTAATGCTCTCCGA 120
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LOCUS      Hepatitis C virus isolate JK030 gene for core, env, and part of
DEFINITION E2/NS1, partial cds.
ACCESSION D49747
VERSION    D49747.1 GI:1197102
KEYWORDS   core, env, and part of E2/NS1.
SOURCE     Hepatitis C virus
ORGANISM   Hepatitis C virus
REFERENCE 1 (sites)
AUTHORS    Tokita,H., Okamoto,H., Iizuka,H., Kishimoto,J., Tsuda,F.,
           Lesmana,L.A., Miyakawa,Y. and Mayumi,M.
TITLE      Hepatitis C virus variants from Jakarta, Indonesia classifiable
           into novel genotypes in the second (2e and 2f), tenth (10a) and
           eleventh (11a) genetic groups
JOURNAL    J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
MEDLINE    96226020
PUBMED     8627233
REFERENCE 2 (bases 1 to 1584)
AUTHORS    Okamoto,H.
JOURNAL    Unpublished
REFERENCE 3 (bases 1 to 1584)
AUTHORS    Okamoto,H.
JOURNAL    Direct Submission
TITLE      Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
           Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
           329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
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DEFINITION E2/NS1, partial cds.
ACCESSION D49753
VERSION    D49753.1 GI:1197124
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SOURCE     Hepatitis C virus
ORGANISM   Hepatitis C virus
REFERENCE 1 (sites)
AUTHORS    Tokita,H., Okamoto,H., Iizuka,H., Kishimoto,J., Tsuda,F.,
           Lesmana,L.A., Miyakawa,Y. and Mayumi,M.
TITLE      Hepatitis C virus variants from Jakarta, Indonesia classifiable
           into novel genotypes in the second (2e and 2f), tenth (10a) and
           eleventh (11a) genetic groups
JOURNAL    J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
MEDLINE    96226020
PUBMED     8627233
REFERENCE 2 (bases 1 to 1584)
AUTHORS    Okamoto,H.
JOURNAL    Unpublished
REFERENCE 3 (bases 1 to 1584)
AUTHORS    Okamoto,H.
JOURNAL    Direct Submission
TITLE      Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
           Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
           329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
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Db 1237 ACTGTTCAGGAGTGCAACTGTTCCATC 1263
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RESULT 10

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LOCUS          Hepatitis C virus (individual isolate fd-3/93) gene for polyprotein
DEFINITION     precursor, partial cds (core protein (carboxy terminus) and E1
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ACCESSION      D30046
VERSION        D30046.1 GI:485798
KEYWORDS       E1 envelope protein; core protein.
SOURCE         Hepatitis C virus
ORGANISM       Hepatitis C virus
                Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                Hepacivirus.
REFERENCE      1 (sites)
AUTHORS        Hotta,H., Handajani,R., Lusida,M.I., Soemarto,W., Doi,H.,
                Miyajima,H. and Homma,M.
TITLE          Subtype analysis of hepatitis C virus in Indonesia on the basis of
                NS5b region sequences
JOURNAL        J. Clin. Microbiol. 32 (12), 3049-3051 (1994)
MEDLINE        95189942
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PUBMED
REFERENCE
AUTHORS
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

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7883898
2 (bases 1 to 411)
Hotta,H.
Unpublished
3 (bases 1 to 411)
Hotta,H.
Direct Submission
Submitted (28-APR-1994) Hak Hotta, Kobe University School of
Medicine, Department of Microbiology; 7-5-1 Kusunoki-cho, Chuo-ku,
Kobe, Hyogo 650, Japan (Tel:078-341-7451(ex.3301),
Fax:078-351-6347)
Submitted (28-Apr-1994) to DDBJ by:
Hak Hotta
Kobe University School of Medicine
Department of Microbiology
7-5-1 Kusunoki-cho, Chuo-ku
Kobe, Hyogo 650
Japan
Phone: 078-341-7451 x3301
Fax: 078-351-6347.
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COMMENT

Direct Submission
Submitted (28-APR-1994) Hak Hotta, Kobe University School of
Medicine, Department of Microbiology; 7-5-1 Kusunoki-cho, Chuo-ku,
Kobe, Hyogo 650, Japan (Tel:078-341-7451(ex.3301),
Fax:078-351-6347)
Submitted (28-Apr-1994) to DDBJ by:
Hak Hotta
Kobe University School of Medicine
Department of Microbiology
7-5-1 Kusunoki-cho, Chuo-ku
Kobe, Hyogo 650
Japan
Phone: 078-341-7451 x3301
Fax: 078-351-6347.

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Qy 428 AGGACTGCAACTGTTCCATC 447
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RESULT 11

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DEFINITION Hepatitis C virus RNA for core, env, and part of E2/NS1 polyprotein.
ACCESSION  D16614
VERSION    D16614.1 GI:475866
KEYWORDS  E2/NS1; core protein; envelope protein.
SOURCE    Hepatitis C virus
ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE  1 (sites)
AUTHORS   Shrestha,S.M., Tsuda,F., Okamoto,H., Tokita,H., Horikita,M.,
            Tanaka,T., Miyakawa,Y. and Mayumi,M.
TITLE     Hepatitis B virus subtypes and hepatitis C virus genotypes in
            patients with chronic liver disease in Nepal
JOURNAL   Hepatology 19 (4), 805-809 (1994)
MEDLINE   94186155
PUBMED    8138250
REFERENCE  2 (sites)
AUTHORS   Tokita,H., Shrestha,S.M., Okamoto,H., Sakamoto,M., Horikita,M.,
            Iizuka,H., Shrestha,S., Miyakawa,Y. and Mayumi,M.
TITLE     Hepatitis C virus variants from Nepal with novel genotypes and
            their classification into the third major group
JOURNAL   J. Gen. Virol. 75 (Pt 4), 931-936 (1994)
MEDLINE   94201770
PUBMED    8151307
COMMENT   Submitted (06-JUL-1993) to DDBJ by:
            Hiroaki Okamoto
            Immunology Division
            Jichi Medical School
            Kawachi-gun
            Tochigi-ken 329-04
            Japan
            Phone: 0285-44-2111 x3334
            Fax: 0285-44-1557.
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Best Local Similarity 73.6%; Pred. No. 1e-57;
Matches 326; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
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QY      61  GCTTTGTTCTCATGCTTGTCTTACACCCACAGCCGGCTGGAGTACCGTAAATGCTCGGA 120
Db      798 GCTCTCTCTCATGCTTGGTTTCCCGCGAGCGGGGTAGATACAGGAACAACGTCGGC 857
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QY      241 ATCCCTGTGAGCCCVACCGTCGCGTGAAGTCGCGCTCGCGCCCTGCGCCACCGCTCTCCGC 300
Db      978 ACGCAGTAACACCGACAGTGGCTGTCAAACATCTGCGCGAGTCACCGCAATCAATCCGC 1037
QY      301 ACGCAGTGGATATGATGTTGGGCGCGCCACCCCTATGCTCAGCTCTCTACGTAGGAGAC 360
Db      1038 AGGCATGTGGATTTGATGTTGGTGGTGCAGCCACGCTGTGTTTCAGCACTCTATGTTGGAGAT 1097
QY      361 CTTTGTGAGCGCTATTCTTCTGTGGCAGGGGTTCTCATGGAGACATCGCCAGCATGG 420
Db      1098 TTGTGCGGGCTGTTTCTTGTGGGCAAGCGTTCACTTTTCAGAGTCGCGCAACATTAT 1157
QY      421 ACTCTCCAGGACTGCAACTGTTC 443
Db      1158 ACCGTCCAGTTGTGCAATTGCTC 1180
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LOCUS     HPCNE274I      1505 bp      RNA      linear      VRL 10-JUN-1999
DEFINITION Hepatitis C virus RNA for core, env, and part of E2/NS1 polyprotein.
ACCESSION  D16620
VERSION    D16620.1 GI:475878
KEYWORDS  E2/NS1; core protein; envelope protein.
SOURCE    Hepatitis C virus
ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE  1 (sites)
AUTHORS   Shrestha,S.M., Tsuda,F., Okamoto,H., Tokita,H., Horikita,M.,
            Tanaka,T., Miyakawa,Y. and Mayumi,M.
TITLE     Hepatitis B virus subtypes and hepatitis C virus genotypes in
            patients with chronic liver disease in Nepal
JOURNAL   Hepatology 19 (4), 805-809 (1994)
MEDLINE   94186155
PUBMED    8138250
REFERENCE  2 (sites)
AUTHORS   Tokita,H., Shrestha,S.M., Okamoto,H., Sakamoto,M., Horikita,M.,
            Iizuka,H., Shrestha,S., Miyakawa,Y. and Mayumi,M.
TITLE     Hepatitis C virus variants from Nepal with novel genotypes and
            their classification into the third major group
JOURNAL   J. Gen. Virol. 75 (Pt 4), 931-936 (1994)
MEDLINE   94201770
PUBMED    8151307
COMMENT   Submitted (06-JUL-1993) to DDBJ by:
            Hiroaki Okamoto
            Immunology Division
            Jichi Medical School
            Kawachi-gun
            Tochigi-ken 329-04
            Japan
            Phone: 0285-44-2111 x3334
            Fax: 0285-44-1557.
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Best Local Similarity 72.9%; Pred. No. 9.5e-57;
Matches 323; Conservative 1; Mismatches 119; Indels 0; Gaps 0;

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Qy 61 GCTTTGTTCTCATGCTTCTTACACCCACAGCGGGCTGGAGTACCGTAATGCTCCGGA 120
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Qy 361 CTTTGTGAGCGCTATTCTTGTGGGAGGGGTTCTCATGGAGACATCGCGCAGATTGG 420
Db 1098 ATGTGTGAGCGCTCTTCTGTTGGGACAGGCTTTTCACTTTCAGACCTCGTCAGCAAC 1157

Qy 421 ACTGTCCAGGACTGCACTGTTTC 443
Db 1158 ACGTGCAGACCTGCAATGCTC 1180

RESULT 13

HPCHCV048
LOCUS HPCHCV048 867 bp RNA linear VRL 15-FEB-2003
DEFINITION Hepatitis C virus DNA, clone:BA-1.
ACCESSION D16736
VERSION D16736.1 GI:506254
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE

1 Ono,T.
AUTHORS
TITLE Hepatitis C virus
JOURNAL Thesis (1993) The University of Tokyo
REFERENCE 2 (bases 1 to 867)
AUTHORS Ono,T.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-1993) Tomoyoshi Ono, Nagoya City University
Medical School, Second Department of Internal Medicine; 1-1
Kawasumi, Mizuho, Nagoya, Aichi 467, Japan
(Tel:052-851-5511(ex.8748,2265), Fax:052-852-0849)
Location/Qualifiers

FEATURES

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Db 425 GCTCTTCTCTCTGCTGACTTGGCCCGCATCTGCTCTGGAGTACAGGAACGCTCCGC 484

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RESULT 14

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ACCESSION D16616
VERSION D16616.1 GI:475870
KEYWORDS E2/NS1: core protein; envelope protein.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE

1 (sites)
AUTHORS Shrestha,S.M., Tsuda,F., Okamoto,H., Tokita,H., Horikita,M.,
Tanaka,T., Miyakawa,Y. and Mayumi,M.
TITLE Hepatitis B virus subtypes and hepatitis C virus genotypes in
patients with chronic liver disease in Nepal
JOURNAL Hepatology 19 (4), 805-809 (1994)
MEDLINE 94186155
PUBMED 8138250
REFERENCE 2 (sites)
AUTHORS Tokita,H., Shrestha,S.M., Okamoto,H., Sakamoto,M., Horikita,M.,
Iizuka,H., Shrestha,S., Miyakawa,Y. and Mayumi,M.
TITLE Hepatitis C virus variants from Nepal with novel
genotypes and their classification into the third major group
J. Gen. Virol. 75 (Pt 4), 931-936 (1994)
94201770

JOURNAL

MEDLINE 8151307
PUBMED
COMMENT Submitted (06-JUL-1993) to DDBJ by:
Hiroaki Okamoto
Immunology Division
Jichi Medical School
Kawachi-gun

Tochigi-ken 329-04 Japan Phone: 0285-44-2111 x3334 Fax: 0285-44-1557. Location/Qualifiers 1. .1504 /organism="Hepatitis C virus" /mol_type="genomic RNA" /isolate="NE137" /db_xref="taxon:11103" <1. .259 /evidence=not_experimental 260. >1504 /codon_start=1 /evidence=not_experimental /product="core, env, and part of E2/NS1" /protein_id="BAA04038.1" /db_xref="GI:475871" translation="MSTLPKPOQTNRNTPRRPQNVKFPGGQIVGGVVLPRRGPRL GYRAVKTSSRQPRKQPIPKAREGRSQAQPGYWPPLYNGECGWAGWLLSPRG SRFSWGNDFRRNRNLGVITLTGCFADLMGYIPLIGAPVGGVARALAHGVRALD GVNATGNLPGCSFSFLALFSLCTCPASGLEVRNTSLGYLVTNDCSNQSIVYADE VILHPCGVPCVATNTSCWTPVSPVAVKHLGATTASIRSHVDMVLAATLCSALY VGLDCCAVLGVQAFVSPRRHATVQTCNSIYPGHSIQRHAWMDMMWNSPAGLAV SHLMRLPQTFEFLIAGAHGVWAGLAYFSMQGNWAKVGLIVLIMFSGVDAETHVTGGTV ASGASLITRPFNSGPKQLQLVN"	
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QY 917	ATCTTGCACTTACCCGGATGTGTCCTCGGTGCACTGCACTGCCAACCAACATCGTCTGG 976
QY 241	ATCCCTGTGAGCCYVACCGTGCCTGAAGTGCCTCGCCGCGCACCGCCTCTCTCCGC 300
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QY 361	CTTTGTGAGCGCTATTCTTGTGTGGCAGGGTTCTCATGGAGACATCCCGCAGCATGG 420
Db	
QY 1097	CTTTGGGGGGGTGTTCTTAGTGGGACACGCGTTCACTTCAGCCCTCGCCGCGCATGG 1156
Db	
QY 421	ACTGTCCAGGACTGCAACTGTTCCAT 446
Db	
QY 1157	ACTGTACAGACATGCAACTGCTCGAT 1182
Db	
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SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED FEATURES source	
Hepatitis C virus type 3a Hepatitis C virus type 3a Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus. 1 (bases 1 to 447) van Doorn,L.J., Kleter,B., Stuyver,L., Maertens,G., Brouwer,H., Schalm,S., Heijtkink,R. and Quint,W. Analysis of hepatitis C virus genotypes by a line probe assay and correlation with antibody profiles J. Hepatol. 21 (1), 122-129 (1994) 95052487 7525693 2 (bases 1 to 447) van Doorn,L.J., Kleter,G.E., Stuyver,L., Maertens,G., Brouwer,J.T., Schalm,S.W., Heijtkink,R.A. and Quint,W.G. Sequence analysis of hepatitis C virus genotypes 1 to 5 reveals multiple novel subtypes in the Benelux countries J. Gen. Virol. 76 (Pt 7), 1871-1876 (1995) 97201609 9049395 Location/Qualifiers 1. .447 /organism="Hepatitis C virus type 3a" /mol_type="genomic RNA" /db_xref="taxon:31652" /clone="NL26" /note="genotype: 3a" <1. .447 /codon_start=1 /product="precursor protein" /protein_id="AAA67821.1" /db_xref="GI:845460" translation="DGINFATGNLPCSPSIFLLALFSLIHPAASLEWRNVSGLYIL TNDCSNLSIVYEDADVILHTPGICPCVQDGNVSTCTWTPVTPVAVKVGATTAIRSH VDLLVGAAATWCSALYVGMCMGAVFLVQAQATFPFRRHQTVQTCNSL"	
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QY 61	GCTTTGTTCTCATGCTTGTCTTACACCACAGCGGGCTGGAGTACCGTAATGCTCCCGGA 120
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QY 301	AGTCATGFGACCTGCTAGTGGCGCGCCACGATGTGCTCTGCGCTCTACGTGGGTGAT 360
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Qy 421 ACTGTCCAGGACTGCAACTGTTC 443

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	233	52.1	541	4	US-09-878-281A-15
6	233	52.1	541	4	US-09-878-281A-21
7	233	52.1	541	4	US-09-878-281A-25
8	233	52.1	541	4	US-09-878-281A-27
9	233	52.1	630	3	US-08-612-973-29
10	233	52.1	630	3	US-08-927-597-29
11	231.4	51.8	541	4	US-09-878-281A-23
12	217.4	48.6	579	4	US-09-878-281A-177
13	215.8	48.3	574	4	US-09-878-281A-120
14	215.8	48.3	579	4	US-09-878-281A-175
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17	209	46.8	447	3	US-08-836-075A-31
18	208.6	46.7	447	3	US-08-836-075A-37
19	206.6	46.2	579	4	US-09-878-281A-173
20	206.2	46.1	579	4	US-09-878-281A-187
21	205	45.9	579	4	US-09-878-281A-171
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23	204.2	45.7	2116	3	US-08-191-160-21
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25	201.4	45.1	579	4	US-09-878-281A-155
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34	196.2	43.9	501	2	US-08-483-695-30	Sequence 30, Appl
35	196.2	43.9	501	2	US-07-965-285-30	Sequence 30, Appl
36	196.2	43.9	501	2	US-08-487-231-30	Sequence 30, Appl
37	196.2	43.9	501	2	US-09-201-912-30	Sequence 30, Appl
38	196.2	43.9	633	3	US-08-612-973-7	Sequence 7, Appl
39	196.2	43.9	633	3	US-08-927-597-7	Sequence 7, Appl
40	196.2	43.9	795	3	US-08-612-973-5	Sequence 5, Appl
41	196.2	43.9	795	3	US-08-927-597-5	Sequence 5, Appl
42	196.2	43.9	2082	3	US-08-612-973-47	Sequence 47, Appl
43	196.2	43.9	2082	3	US-08-927-597-47	Sequence 47, Appl
44	196.2	43.9	2433	3	US-08-612-973-49	Sequence 49, Appl
45	196.2	43.9	2433	3	US-08-927-597-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-08-836-075A-51

; Sequence 51, Application US/08836075A

; Patent No. 6180768

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT

; APPLICANT: STUYVER, LIEVEN

; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES

; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC

; TITLE OF INVENTION: AGENTS

; NUMBER OF SEQUENCES: 207

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARNOLD, WHITE & DURKEE

; STREET: P.O. BOX 4433

; CITY: HOUSTON

; STATE: TEXAS

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Microsoft Word 6.0 / ASCII text output

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/836, 075A

; FILING DATE: 21 Apr 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP95/04155

; FILING DATE: 23 Oct 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 94870166.9

; FILING DATE: 21 Oct 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95870076.7

; FILING DATE: 28 Jun 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KAMMERER, PATRICIA A.

; REGISTRATION NUMBER: 29,775

; REFERENCE/DOCKET NUMBER: INNS:004

; INFORMATION FOR SEQ ID NO: 51:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 447 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-836-075A-51

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Query Match 99.7%; Score 445.8; DB 3; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.9e-124;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTTGCTCTTCTCTATCTTCTCTG 60
Db 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTTGCTCTTCTCTATCTTCTCTG 60

QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCCGGCTGGAGTACCGTAATGCTCCGGA 120
Db 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCCGGCTGGAGTACCGTAATGCTCCGGA 120

QY 121 CTCTACATGGTAATAACGACTGAGTAACGCTAGTATCGTGTATGAGCCCGGGATATT 180
Db 121 CTCTACATGGTAATAACGACTGAGTAACGCTAGTATCGTGTATGAGCCCGGGATATT 180

QY 181 ATCCTCCACTTACCTGGCTGTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 ATCCTCCACTTACCTGGCTGTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

QY 241 ATCCCTGTGAGCCYACCGTGGCGCTGAAAGTCCGCTGGCCGCGCCACCGCTCTCTCCGC 300
Db 241 ATCCCTGTGAGCCYACCGTGGCGCTGAAAGTCCGCTGGCCGCGCCACCGCTCTCTCCGC 300

QY 301 ACCCAGCTGATATGATGGTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAGAGAC 360
Db 301 ACCCAGCTGATATGATGGTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAGAGAC 360

QY 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGTTCTCATGGAGACATCGCCAGCATGG 420
Db 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGTTCTCATGGAGACATCGCCAGCATGG 420

QY 421 ACTGTCCAGGACTGCAACTGTTCCATC 447
Db 421 ACTGTCCAGGACTGCAACTGTTCCATC 447

RESULT 2
US-09-878-281A-13
; Sequence 13, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
; FILE REFERENCE: 35
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-13

Query Match 52.8%; Score 236.2; DB 4; Length 541;
Best Local Similarity 70.7%; Pred. No. 2.9e-61;
Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTTGCTCTTCTCTATCTTCTCTG 60
Db 62 GACGGGATAAATTTTCGCAACAGGGAATTTGCGCGTTGCTCTTCTCTATCTTCTCTT 121

QY 61 GCTTTGTTCTCATGCTTGTCTTACCCACAGCCGGCTGGAGTACCGTAATGCTCCGGA 120
Db 122 GCTCTGTTCTCTTGTCTTAAATCCATCCAGAGTAGTCTAGAGTGGCGGAACAGTCTGGC 181

QY 121 CTCTACATGGTAATAACGACTGAGTAACGCTAGTATCGTGTATGAGCCCGGGATATT 180
Db 182 CTCTATGCTTACCAACGACTGTTCCAAATAGCAGTATTTGTATGAGCCCGGATGCGTT 241

QY 181 ATCCTCCACTTACCTGGCTGTGCTCCCTGCTGCTGCTCTGCGCAATACATCAAGATGCTGG 240
Db 242 ATCTGCAACACACCGGCTGTGTACCTTGTGTTTCAGGACGGTAATACATCTGCGTCTGG 301

QY 241 ATCCCTGTGAGCCYACCGTGGCGCTGAAAGTCCGCTGGCCGCGCCACCGCTCTCTCCGC 300
Db 302 ACCCAGTGTACCTACAGTGGCAGTACGGTACGTCGAGCAACCCACCGCTTCGATACGC 361

QY 301 ACCCAGTGTATGATGGTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAGAGAC 360
Db 362 AGGCAATGTAGACATATTTGGGCGGCCACGATGTCTCTCTCTACGTGGGTGAT 421

QY 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGTTCTCATGGAGACATCGCCAGCATGG 420
Db 422 ATGTGTGGGCGCTCTTCTCTGCGGACAAGCCTTCAGCTTCAGACCTCGTCCCATCAA 481

QY 421 ACTGTCCAGGACTGCAACTGTTTC 443
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Db 242 ATTCTGCACACACCGGCTGTGTACTTGTGTTCAGGACGGTAATACATCTGCGTGTGG 301
QY 241 ATCCCTGTGAGCCYACCGTGGCGCTGAAAGTCCGCTGGCCGCGCCACCGCTCTCTCCGC 300
Db 302 ACCCAGTGTACACCTACAGTGGCAGTACGGTACGTCGAGCAACCCACCGCTTCGATACGC 361
QY 301 ACCCAGTGGATATGATGGTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAGAGAC 360
Db 362 AGGCAATGTAGACATGTTGTGGGCGGCCACGATGTCTCTCTCTACGTGGGTGAT 421
QY 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGTTCTCATGGAGACATCGCCAGCATGG 420
Db 422 ATGTGTGGGCGCTCTTCTCTGCGGACAAGCCTTCAGTTTCAGACCTCGTCCCATCAA 481
QY 421 ACTGTCCAGGACTGCAACTGTTTC 443
Db 482 ACGTCCAGACCTGTAACTGCTC 504

RESULT 3
US-09-878-281A-17
; Sequence 17, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
; FILE REFERENCE: 35
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-17

Query Match 52.8%; Score 236.2; DB 4; Length 541;
Best Local Similarity 70.7%; Pred. No. 2.9e-61;
Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTTCGCAACAGGGAATTTACCTGGTTGCTCTTCTCTATCTTCTCTG 60
Db 62 GACGGGATAAATTTTCGCAACAGGGAATTTGCGCGTTGCTCTTCTCTATCTTCTCTT 121

QY 61 GCTTTGTTCTCATGCTTGTCTTACCCACAGCCGGCTGGAGTACCGTAATGCTCCGGA 120
Db 122 GCTCTGTTCTCTTGTCTTAAATCCATCCAGAGTAGTCTAGAGTGGCGGAACAGTCTGGC 181

QY 121 CTCTACATGGTAATAACGACTGAGTAACGCTAGTATCGTGTATGAGCCCGGGATATT 180
Db 182 CTCTACGTCCTTACCAACGACTGTTCCAAATAGCAGTATTTGTATGAGCCCGGATGCGTT 241

QY 181 ATCCTCCACTTACCTGGCTGTGCTCCCTGCTGCTGCTCTGCGCAATACATCAAGATGCTGG 240
Db 242 ATCTGCAACACACCGGCTGTGTACCTTGTGTTTCAGGACGGTAATACATCTGCGTCTGG 301

QY 241 ATCCCTGTGAGCCYACCGTGGCGCTGAAAGTCCGCTGGCCGCGCCACCGCTCTCTCCGC 300
Db 302 ACCCAGTGTACCTACAGTGGCAGTACGGTACGTCGAGCAACCCACCGCTTCGATACGC 361

QY 301 ACCCAGTGTATGATGGTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAGAGAC 360
Db 362 AGGCAATGTAGACATATTTGGGCGGCCACGATGTCTCTCTCTACGTGGGTGAT 421

QY 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGTTCTCATGGAGACATCGCCAGCATGG 420
Db 422 ATGTGTGGGCGCTCTTCTCTGCGGACAAGCCTTCAGCTTCAGACCTCGTCCCATCAA 481

QY 421 ACTGTCCAGGACTGCAACTGTTTC 443
```

Db 482 ACGTCCAGACCTGTAAGTCTC 504

RESULT 4

```

US-09-878-281A-19
; Sequence 19, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: New sequences of hepat
; TITLE OF INVENTION: and therapy
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-19

```

Query Match 52.5%; Score 234.6; DB 4; Length 541;
Best Local Similarity 70.4%; Pred. No. 8.9e-61;
Matches 312; Conservative 1; Mismatches 130; Indels 0; Gaps 0;

Qy	1	GACGGAAATTAATTTGCGAACAGGGAATTA	CTCGTGGTGGCTCTTTCTCTATCTCTCCATCTCG	60
Db	62	GACGGGATAAATTTGCGAACAGGGAATTTG	CCGGTTGCTCTTTTCTATATTTTCTTTCTT	121
Qy	61	GCTTTGTTCATGCTTGCTTACACCCACAGC	CCGGCTGGAGTAGCCTAATGCTCCGGGA	120
Db	122	GCTCTGTTCTTCTGTTAATTCATCCAGACG	TAGTCTAGAGTGGCGGAATAGTCTGGC	181
Qy	121	CTCTACATGGTAATCAACGAGTCGAGTAAC	CGGTAGTATCGGTATAGAGCGCGGGGATAT	180
Db	182	CTCTATGTCTTTACCAACGAGCTGTTTCCA	ATAGCAGTATTTGTACGAGGCGGATGACGTT	241
Qy	181	ATCTCTCCAGTACCTCTGGCTGTGCCCTCG	TACGCTCTGCGCAATACATCAAGATGCTGG	240
Db	242	ATTCTGCACACACCCGGCTGCNATCTTGTG	TCAGGACGGCAATACATCCAGCTGCTGG	301
Qy	241	ATCCCTGTGAGCCYACCGTGCCTGAAAGTC	GCCTCGCGCGCACCGCTCTCTCCCG	300
Db	302	ACCCAGTGCACCTTACAGTGGCAGTCAAGT	TACGTTCGGAGCAACCCGCTTCGATACGC	361
Qy	301	AGCAGCTGGATAGATGGTGGGCGCGCACCT	TATGCTCAGCTCTCTAGGTAGAGAC	360
Db	362	AGTCATGTGGACCTATTAGTGGGCGCGCCAC	GATGTGCTCAGCGCTCTACGTGGGTGAT	421
Qy	361	CTTTGTGGAGCGCTATTTCTTGTG	GGGCGAGGGGTTCTCATGGAGACATCCCGACGAT	420
Db	422	ATGTGTGGGCGCGTCTTCTTGTGGGAC	AGCCTTCAGTTTCAGACCTCGTCCCGCATCAA	481
Qy	421	ACTGTCCAGGACTGCAACTGTTC	443	
Db	482	ACGGTCCAGACCTGTAACTGTCTC	504	

RESULT 5

```

US-09-878-281A-15
; Sequence 15, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis
; TITLE OF INVENTION: and therapy
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15

```

```

Query Match          52.1%; Score 233; DB 4; Length 541;
Best Local Similarity 70.2%; Pred. No. 2.7e-60;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

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[illegible]

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; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-15

```

Query Match	52.1%;	Score 233;	DB 4;	Length 541;	
Best Local Similarity	70.2%;	Ref. No. 2.7e-60;			
Matches 311;	Conservative	1;	Mismatches 131;	Indels 0;	Gaps 0;
1	y	GACGGAATTAATTTTCGCAACAGGGAATTTACCTGGTTGCTCTTTCTCTATCTTCTCTCTG 60			
62	b	GACGGGATAAATTTTCGCAACAGGGAATTTGCCGGTTGCTCTCTTTCTATCTTCTCTTCT 121			
61	y	GCTTTGTCTCATGCTTTCGTTTACCCACACCGCGGCTGGAGTACCGTAATGCTCTCCGGA 120			
122	b	GCTCTGTTTCTCTTGTCTTAATCCATCCACGACGCTAGCTAGAGTGGCGGAACACGCTGTGGC 181			
121	y	CTCTACATGGTAATTAACGCACTTCGCAAGTAAACGGTAGTATCGTGTATGAGCGCGGGGATATT 180			
182	b	CTCTATGTCCTTTACCAACGACTGTTTCCAATAGCAGTATTGTGTATGAGCGCGATGACGTT 241			
181	y	ATCCTTCCACTTACCTGGCTGTGTCCCTGGCTAGCCTCTGGCAATACATCAAGATGCTGG 240			
242	b	ATTCTGCAACACACCCGGCTGTGTACCTTGTGTTCAGGACGGTAATATACATCTGCGTGTCTGG 301			
241	y	ATCCCTGTGAGCCCVACCGTCCGCTGAAGTCGCCCTGCGCGGCCACCGCCTCTCTCCGC 300			
302	b	ACCCAGTGCACCTTACAGTGGCAGTCAAGTACGTCCGAGGCAACCAACGCTTCGATACGC 361			
301	y	ACGCAACGTGGATATGATGGTGGGRCGGCCACCCCTATGCTCAGTCTCTTACGTAGGAGAC 360			
362	b	AGGCATGTAGACATATTTGGTGGCGCGGCCCAATATGTCTCTCTACGTGGGGTGAT 421			
361	y	CTTTCTGGAGCGCTATTTCTTGTGTTGGGACGGGTTCTCATGGAGACATCGCCACGATTGG 420			
422	b	ATGTGTGGGCGCTTCTCTCTGTGGGCAACGCTTTCAGTTTCAGACCTCTGTGGCCATCAA 481			
421	y	ACTGTCCAGGACTGCAACTGTTCC 443			
482	b	ACGGTCCAGACCTGTAACTGCTC 504			

RESULT 6

```

US-09-878-281A-21
; Sequence 21, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis
; TITLE OF INVENTION: and therapy
; FILE REFERENCES: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-21

```

Query Match	52.1%;	Score 233;	DB 4;	Length 541;
Best Local Similarity	70.2%;	Pred. No. 2.7e-60;		
Matches 311;	Conservative 1;	Mismatches 131;	Indels 0;	Gaps 0;
1	GACGGAAATTAAATTCGCAACAGGGAATTTACCTGGTTGCTCTTTCTCTATCTTCTCTTCG	60		
62	GACGGGATAAAATTCGCAACAGGGAATTTGCCGGTTGCTCCTTTCTATTTTCTCTTCT	121		
61	GCTTTTCTTCATGCTTGCTTACCCACAGCGGGCTGGAGTACCGTAATGCTCCCGA	120		
122	GCTCTGCTCTCTTGCTTAATTCATCCAGCACTAGCTAGAGTGGCGGAATACGTCTGC	181		

```
QY 121 CTCTACATGGTAACCTAACGACTACAGTAACGGTAGTAGTCGTGTATGAGCGCGGGATATT 180
Db 182 CTCATATGCTCTTACCAACGACTGTTCCAATAGCAGTAATTGTTAGAGGCGGATGACGTT 241
QY 181 ATCCCTCCACTTACCTGGCTGTGTCCTCGCTGCGTACGCTCTGCGCAATACATCAAGATGCTGG 240
Db 242 ATTCTGCACACACCGCGCTGATACCTTTGTCTCAGGACGCGCAATACATCCAGTGTCTGG 301
QY 241 ATCCCTGTGAGCCVACCGTGCCTGAGTCGCGCTCGCGCCCGCCAGCGCTCTCTCCGC 300
Db 302 ACCCCAGTGACACTACAGTGGCAGTCAAGTACGTCGAGCAACCCGCTTCGATACGC 361
QY 301 AGCAGCGTGATATGATGGTGGGCGCGCCACCCCTATGCTCAGCTCTCTACGTAGGAGAC 360
Db 362 AGTCATGTGACCTATTAGTGGCGCGCCAGGATGTCTCTGGCTCTACGTGGGTGAC 421
QY 361 CTTTGTGGAGCGCTATTCTTGTGTGGCAGGGGTTCTCATGGAGACATCCCGAGCAATTGG 420
Db 422 ATGTGTGGGGTGTCTTCTCGTGGGCAAGCCCTTCACGTTCCAGACCTGTCGCCATCAA 481
QY 421 ACTGTCCAGGACTGCAACTGTTC 443
Db 482 ACGGTCCAGCTGTAACGTCTC 504

RESULT 7
US-09-878-281A-25
; Sequence 25, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Imogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25
; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-25

Query Match 52.1%; Score 233; DB 4; Length 541;
Best Local Similarity 70.2%; Pred. No. 2.7e-60;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAAATTAATTTCGCAACAGGAAATTTACCTGGTGTGCTCTTCTCTATCTCTCTCTG 60
Db 62 GACGGATAAACTTCGCAACAGGAAATTTGCCCGGTGTCTCTTTCTATCTCTCTCTT 121
QY 61 GCTTTGTCTCATGCTTGTCTTACCCACAGCGCGGCTGGAGTACCGTAATGCTTCGGGA 120
Db 122 GCTCTGTCTTCTTGTCTTAAATCCATCCAGCAGCTGTCTAGAGTGGCGGAATAGCTGGC 181
QY 121 CTCTACATGGTAACCTAACGACTACAGTAACGGTAGTAGTCGTGTATGAGCGCGGGATATT 180
Db 182 CTCATGTCTTCTTGTCTTAAATCCATCCAGCAGCTGTCTTCTATCTCTCTCTCTCT 241
QY 181 ATCCCTCCACTTACCTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 242 ATTCTGCACGCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
QY 241 ATCCCTGTGAGCCVACCGTGCCTGAGTGGCGCGCGCCAGCGCTCTCTCTCCGC 300
Db 302 ACCCCAGTAACCTACAGTGGCAGTCAAGTACGTCGAGCAACCCGCTTCGATACGC 361
QY 301 AGCAGCGTGATATGATGGTGGGCGCGCCACCCCTATGCTCAGCTCTCTACGTAGGAGAC 360
Db 362 AGTCATGTGACCTATTAGTGGCGCGCCAGGATGTCTCTGGCTTTACGTGGGTGAT 421
QY 361 CTTTGTGGAGCGCTATTCTTGTGTGGCAGGGGTTCTCATGGAGACATCCCGAGCAATTGG 420
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Db 422 ATGTGTGGGGCGCTTCTCTGTGGGACAGCCCTTACGTTTCAGACCCCGCGCCATCAA 481
QY 421 ACTGTCCAGGACTGCAACTGTTC 443
Db 482 ACGGTCCAGACTGTAACGTCTC 504

RESULT 8
US-09-878-281A-27
; Sequence 27, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Imogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 27
; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-878-281A-27

Query Match 52.1%; Score 233; DB 4; Length 541;
Best Local Similarity 70.2%; Pred. No. 2.7e-60;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAAATTAATTTCGCAACAGGAAATTTACCTGGTGTGCTCTTCTCTATCTCTCTCTG 60
Db 62 GACGGATAAACTTCGCAACAGGAAATTTGCCCGGTGTCTCTTTCTATCTCTCTCTT 121
QY 61 GCTTTGTCTCATGCTTGTCTTACCCACAGCGCGGCTGGAGTACCGTAATGCTTCGGGA 120
Db 122 GCTCTGTCTTCTTGTCTTAAATCCATCCAGCAGCTGTCTAGAGTGGCGGAATAGCTGGC 181
QY 121 CTCTACATGGTAACCTAACGACTACAGTAACGGTAGTAGTCGTGTATGAGCGCGGGATATT 180
Db 182 CTCATGTCTTCTTGTCTTAAATCCATCCAGCAGCTGTCTTCTATCTCTCTCTCTCT 241
QY 181 ATCCCTCCACTTACCTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 242 ATTCTGCACGCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
QY 241 ATCCCTGTGAGCCVACCGTGCCTGAGTGGCGCGCGCCAGCGCTCTCTCTCCGC 300
Db 302 ACCCCAGTAACCTACAGTGGCAGTCAAGTACGTCGAGCAACCCGCTTCGATACGC 361
QY 301 AGCAGCGTGATATGATGGTGGGCGCGCCACCCCTATGCTCAGCTCTCTACGTAGGAGAC 360
Db 362 AGTCATGTGAGCGCTTGTAGTGGCGCGGCAAGATGTCTCTGCGCTTTACGTGGGTGAT 421
QY 361 CTTTGTGGAGCGCTATTCTTGTGTGGCAGGGGTTCTCATGGAGACATCCCGAGCAATTGG 420
Db 422 ATGTGTGGGGCGCTCTTCTCTGTGGGCAAGCCCTTCACGTTTCAGACCCCGCGCCATCAA 481
QY 421 ACTGTCCAGGACTGCAACTGTTC 443
Db 482 ACGGTCCAGACTGTAACGTCTC 504

RESULT 9
US-08-612-973-29
; Sequence 29, Application US/08612973
; Patent No. 6150134
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
; APPLICANT: BUYSE, MARIE-ANGE
```


;; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
;; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
;; NUMBER OF SEQUENCES: 111
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON & VANDERHUYE P.C.
;; STREET: 1100 NORTH GLEBE ROAD
;; CITY: ARLINGTON
;; STATE: VIRGINIA
;; COUNTRY: U.S.A.
;; ZIP: 22201-4714

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/612,973
;; FILING DATE: 11-MAR-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BYRNE, THOMAS E.
;; REGISTRATION NUMBER: 32,205
;; REFERENCE/DOCKET NUMBER: 1487-10

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 630 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear

;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..627

;; FEATURE:
;; NAME/KEY: mat_peptide
;; LOCATION: 1..624
US-08-612-973-29

Query Match 52.1%; Score 233; DB 3; Length 630;
Best Local Similarity 70.2%; Pred. No. 2.9e-60;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTTGCTCTTCTCTATCTTCTCTG 60
DB 124 GACGGGATAAATTCGCAACAGGGAATTTGCCGGTTGCTCTTCTATTTCTCTCTC 183

QY 61 GCTTTGTTCTCATGCTTACACCAAGCGGGCTGGAGTACCGTAATGCTTCCGGA 120
DB 184 GCTCTGTTCTCTTCTTAATTCATCCAGCAGTAGTCTAGAGTGGCGGAATACGCTGCG 243

QY 121 CTCTACATGGTAACCTAACGACTGACGTACCGTAGTATCGTGTATGAGCCGGGATATT 180
DB 244 CTCTATGTCCTTACCAACAGCTGTTTCCAAATGACGATTTGTGTACGAGCCGATGACGTT 303

QY 181 ATCTCTCCACTTACCTGGCTGTGTCCTCGTACGCTCTGGCAATACATCAAGATGCTGG 240
DB 304 ATCTGCAACACCCGGCTGCAATACCTGTGTCAGGACGGCAATACATCCAGTGTGG 363

QY 241 ATCCCTGTGAGCCVACCGTCCGGTGAAGTCCGCTGCGCCGCGCACCGCTCTCTCCGC 300
DB 364 ACCCCAGTGACACCTACAGTGGCAGTCAAGTACGTGGAGCAACACCGCTTCGATACG 423

QY 301 AGCAGTGGATATGATGTGGGGCGGCCACCTATGCTAGCTCTCTACGTAGAGAC 360
DB 424 AGTCATGTGGACCTATTAGTGGGGCGGCCACGATGTGCTCTGCGCTCTACGTGGGTGAC 483

QY 361 CTTTGTGAGCGCTATTTCTTCTGCGGAGGGGTTCTCATGAGACATCGCCAGATTGG 420
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DB 484 ATGTGTGGGCTGTCTTCTCTGGGACAGCCTTCACGTTCCAGACCTCGTCCCATCAA 543
QY 421 ACTGTCCAGACTGCAACTGTTTC 443
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RESULT 10

US-08-927-597-29
;; Sequence 29, Application US/08927597
;; Patent No. 6245503
;; GENERAL INFORMATION:
;; APPLICANT: MAERTENS, GEERT
;; APPLICANT: BOSMAN, FONS
;; APPLICANT: DE MARTYNOFF, GUY
;; APPLICANT: BUYSE, MARIE-ANGE

;; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
;; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
;; NUMBER OF SEQUENCES: 111
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON & VANDERHUYE P.C.
;; STREET: 1100 NORTH GLEBE ROAD
;; CITY: ARLINGTON
;; STATE: VIRGINIA
;; COUNTRY: U.S.A.
;; ZIP: 22201-4714

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/927,597
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/612,973
;; FILING DATE: 11-MAR-1996

;; ATTORNEY/AGENT INFORMATION:
;; NAME: BYRNE, THOMAS E.
;; REGISTRATION NUMBER: 32,205
;; REFERENCE/DOCKET NUMBER: 1487-10
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 630 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear

;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..627
;; FEATURE:
;; NAME/KEY: mat_peptide
;; LOCATION: 1..624
US-08-927-597-29

Query Match 52.1%; Score 233; DB 3; Length 630;
Best Local Similarity 70.2%; Pred. No. 2.9e-60;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

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QY 61 GCTTTGTTCTCATGCTTACACCAAGCGGGCTGGAGTACCGTAATGCTTCCGGA 120
DB 184 GCTCTGTTCTCTTCTTAATTCATCCAGCAGTAGTCTAGAGTGGCGGAATACGCTGCG 243

QY 121 CTCTACATGGTAACCTAACGACTGACGTACCGTAGTATCGTGTATGAGCCGGGATATT 180
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QY 241 ATCCCTGTGAGCCVACCGTCCGGTGAAGTCCGCTGCGCCGCGCACCGCTCTCTCCGC 300
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QY 301 AGCAGTGGATATGATGTGGGGCGGCCACCTATGCTAGCTCTCTACGTAGAGAC 360
DB 424 AGTCATGTGGACCTATTAGTGGGGCGGCCACGATGTGCTCTGCGCTCTACGTGGGTGAC 483
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; FILE REFERENCE: 35
 ; CURRENT APPLICATION NUMBER: US/09/878,281A
 ; CURRENT FILING DATE: 2001-06-12
 ; NUMBER OF SEQ ID NOS: 284
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 120
 ; LENGTH: 574
 ; TYPE: DNA
 ; ORGANISM: hepatitis C virus
 US-09-878-281A-120

Query Match 48.3%; Score 215.8; DB 4; Length 574;
 Best Local Similarity 67.3%; Pred. No. 4.2e-55;
 Matches 301; Conservative 2; Mismatches 144; Indels 0; Gaps 0;

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 Qy 121 CTCTACATGTAACGAGCTGAGTAAACGGTAGTATCGTGTATGAGGCCGGGATATT 180
 Db 220 ATTTATCACGTCAACCAAGTACTCCCGAACTCTAGTATAGTGTATGAAGCTGACCAT 279
 Qy 181 ATCTCTCACATTACTGGCTGTGCTCCCTGGTACGCTCTGGCAATACATCAAGATGCTGG 240
 Db 280 ATCATGATCTACAGGGTGTGCTTGGTGAGAACCGGGAACACCTCGCGCTGCTGG 339
 Qy 241 ATCCCTGTGAGCCYACCGTGGCGGTGAAGTCCGCCCGCCACCGCCTCTCTCCGC 300
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 Qy 301 ACGCAGCTGATATGATGTTGGGCGGGCCACCCATGCTCAGCTCTCTACGTAGGAGAC 360
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 Qy 421 ACTGTCAGGACTGCAACTGTTCATC 447
 Db 520 ACTACCCAGGACTGCAACTGCTCTATC 546

RESULT 14
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 ; Sequence 175, Application US/09878281A
 ; Patent No. 6762024
 ; GENERAL INFORMATION:
 ; APPLICANT: Innogenetics N.V.
 ; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy
 ; FILE REFERENCE: 35
 ; CURRENT APPLICATION NUMBER: US/09/878,281A
 ; CURRENT FILING DATE: 2001-06-12
 ; NUMBER OF SEQ ID NOS: 284
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 175
 ; LENGTH: 579
 ; TYPE: DNA
 ; ORGANISM: hepatitis C virus
 US-09-878-281A-175

Query Match 48.3%; Score 215.8; DB 4; Length 579;
 Best Local Similarity 67.3%; Pred. No. 4.2e-55;
 Matches 301; Conservative 2; Mismatches 144; Indels 0; Gaps 0;

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Search completed: March 4, 2005, 14:35:49
Job time : 699 secs

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2005, 11:33:49 ; Search time 19001 Seconds
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Title: US-09-851-138c-51

Perfect score: 447

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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SUMMARIES

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ALIGNMENTS

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 ; APPLICANT: MAERTENS, GIEERT
 ; STUYVER, LIEVEN
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 ; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
 ; AGENTS
 ; NUMBER OF SEQUENCES: 207
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: ARNOLD, WHITE & DURKEE
 ; STREET: P.O. BOX 4433
 ; CITY: HOUSTON
 ; STATE: TEXAS
 ; COUNTRY: USA
 ; ZIP: 77210-4433
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 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Microsoft Word 6.0 / ASCII text output
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/836,075A
 ; FILING DATE: 21-Apr-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP95/04155
 ; FILING DATE: 23 Oct 1995
 ; APPLICATION NUMBER: EP 94870166.9
 ; FILING DATE: 21 Oct 1994
 ; APPLICATION NUMBER: EP 95870076.7
 ; FILING DATE: 28 Jun 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KAMMERER, PATRICIA A.
 ; REGISTRATION NUMBER: 29,775
 ; REFERENCE/DOCKET NUMBER: INNS:004
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 447 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
 ; US-08-836-075A-51
 ;
 ; Query Match 99.7%; Score 445.8; DB 14; Length 447;
 ; Best Local Similarity 100.0%; Pred. No. 1.5e-114;
 ; Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;
 ; QY 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTGTCTTCTTCTATCTTCTCTG 60
 ; DB 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTGTCTTCTTCTATCTTCTG 60
 ; QY 61 GCTTTGTCTCATGCTTGTCTTACCCACAGCGGGCTGGAGTACCGTAATGCTCCGGA 120
 ; DB 61 GCTTTGTCTCATGCTTGTCTTACCCACAGCGGGCTGGAGTACCGTAATGCTCCGGA 120
 ; QY 121 CTCTACATGGTAACCACTGACGTAACGTAAGTATGCTGTATGAGCGGGGATATT 180
 ; DB 121 CTCTACATGGTAACCACTGACGTAACGTAAGTATGCTGTATGAGCGGGGATATT 180
 ; QY 181 ATCCTCCACTTACCTGGCTGTGTCCTCGTACGCTCTGGCAATACATCAAGATGCTGG 240
 ; DB 181 ATCCTCCACTTACCTGGCTGTGTCCTCGTACGCTCTGGCAATACATCAAGATGCTGG 240
 ; QY 241 ATCCCTGTGAGCCCTACCGTCCCGTGAAGTCCCGTCCCGCCACCGCTCTCTCCGC 300
 ; DB 241 ATCCCTGTGAGCCCTACCGTCCCGTGAAGTCCCGTCCCGCCACCGCTCTCTCCGC 300
 ; QY 301 ACGCAGTGGATATGATGTTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAAGAC 360

Db 301 ACCACGTCGATGATGTTGGGCGGCCACCTATGCTCAGCTCTCAGTAGAGAC 360
Qy 361 CTTTGTGGAGCGCTATTCTTGTGGCAGGGTTCTCATGGAGACATGCCAGCATTTG 420
Db 361 CTTTGTGGAGCGCTATTCTTGTGGCAGGGTTCTCATGGAGACATGCCAGCATTTG 420
Qy 421 ACTGTCAGGACTGCAACTGTTCCATC 447
Db 421 ACTGTCAGGACTGCAACTGTTCCATC 447

RESULT 2

US-08-836-075B-51
; Sequence 51, Application US/08836075B
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; FILE OF INVENTION: phylogenetic, therapeutic and diagnostic agents.
; FILE REFERENCE: 2551-105
; CURRENT APPLICATION NUMBER: US/08/836, 075B
; CURRENT FILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: EP 95870076.7
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 51
; LENGTH: 447
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-08-836-075B-51

Query Match 99.7%; Score 445.8; DB 14; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTGTCTCTTCTCTATCTCTCTCTG 60
Db 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTGTCTCTTCTCTATCTCTCTCTG 60
Qy 61 GCTTTGTTCTCATGCTTGTCTTACACCCAGCGGGCTGGAGTACCGTAATGCTCCGGA 120
Db 61 GCTTTGTTCTCATGCTTGTCTTACACCCAGCGGGCTGGAGTACCGTAATGCTCCGGA 120
Qy 121 CTCTACATGTTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGCCGGGGATATT 180
Db 121 CTCTACATGTTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGCCGGGGATATT 180
Qy 181 ATCTCTCACTTACCTGGTGTGTCCTCGGTACGCTCTGGCAATACATCAAGATGCTGG 240
Db 181 ATCTCTCACTTACCTGGTGTGTCCTCGGTACGCTCTGGCAATACATCAAGATGCTGG 240
Qy 241 ATCCCTGTGAGCCYACCGTGCCTGGAAGTCCCTGCGCCGCGCCACCGCTCTCTCCGC 300
Db 241 ATCCCTGTGAGCCYACCGTGCCTGGAAGTCCCTGCGCCGCGCCACCGCTCTCTCCGC 300
Qy 301 ACGCAGTGGATATGATGTTGGGCGGCCACCTATGCTCAGCTCTCTACGTAGGAGAC 360
Db 301 ACGCAGTGGATATGATGTTGGGCGGCCACCTATGCTCAGCTCTCTACGTAGGAGAC 360
Qy 361 CTTTGTGGAGCGCTATTCTTGTGGCAGGGTTCTCATGGAGACATGCCAGCATTTG 420
Db 361 CTTTGTGGAGCGCTATTCTTGTGGCAGGGTTCTCATGGAGACATGCCAGCATTTG 420
Qy 421 ACTGTCAGGACTGCAACTGTTCCATC 447
Db 421 ACTGTCAGGACTGCAACTGTTCCATC 447

RESULT 3

US-09-374-494-51

; Sequence 51, Application US/09374494
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: GENOTYPES AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD WHITE & DURKEE
; STREET: 750 BERING DRIVE
; CITY: HOUSTON
; STATE: TX
; COUNTRY: US
; ZIP: 77057
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/374,494
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNU:004--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713.787.1400
; TELEFAX: 713.787.1440
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-374-494-51

Query Match 99.7%; Score 445.8; DB 21; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTGTCTCTTCTCTATCTCTCTCTG 60
Db 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTGTCTCTTCTCTATCTCTCTCTG 60
Qy 61 GCTTTGTTCTCATGCTTGTCTTACACCCAGCGGGCTGGAGTACCGTAATGCTCCGGA 120
Db 61 GCTTTGTTCTCATGCTTGTCTTACACCCAGCGGGCTGGAGTACCGTAATGCTCCGGA 120
Qy 121 CTCTACATGTTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGCCGGGGATATT 180
Db 121 CTCTACATGTTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGCCGGGGATATT 180
Qy 181 ATCTCTCACTTACCTGGTGTGTCCTCGGTACGCTCTGGCAATACATCAAGATGCTGG 240
Db 181 ATCTCTCACTTACCTGGTGTGTCCTCGGTACGCTCTGGCAATACATCAAGATGCTGG 240
Qy 241 ATCCCTGTGAGCCYACCGTGCCTGGAAGTCCCTGCGCCGCGCCACCGCTCTCTCCGC 300
Db 241 ATCCCTGTGAGCCYACCGTGCCTGGAAGTCCCTGCGCCGCGCCACCGCTCTCTCCGC 300
Qy 301 ACGCAGTGGATATGATGTTGGGCGGCCACCTATGCTCAGCTCTCTACGTAGGAGAC 360
Db 301 ACGCAGTGGATATGATGTTGGGCGGCCACCTATGCTCAGCTCTCTACGTAGGAGAC 360
Qy 361 CTTTGTGGAGCGCTATTCTTGTGGCAGGGTTCTCATGGAGACATGCCAGCATTTG 420
Db 361 CTTTGTGGAGCGCTATTCTTGTGGCAGGGTTCTCATGGAGACATGCCAGCATTTG 420
Qy 421 ACTGTCAGGACTGCAACTGTTCCATC 447

```
Db 421 ACTGTCAGGACTGCAACTGTTCCATC 447
RESULT 4
US-09-374-494A-51
; Sequence 51, Application US/09374494A
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; FILE OF INVENTION: prophylactic, therapeutic and diagnostic agents.
; FILE REFERENCE: 46 USdiv1
; CURRENT APPLICATION NUMBER: US/09/374, 494A
; CURRENT FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: EP 95870076.7
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 447
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-374-494A-51

Query Match 99.7%; Score 445.8; DB 21; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTGGCTCTTCTCTATCTCTCTCTG 60
Db 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTGGCTCTTCTCTATCTCTCTCTG 60

QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCGGGCTGGAGTACCGTAATGCTCCGGA 120
Db 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCGGGCTGGAGTACCGTAATGCTCCGGA 120

QY 121 CTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCGCGGGATATT 180
Db 121 CTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCGCGGGATATT 180

QY 181 ATCCTCCACTTACCTGGCTGTCCCTCGTACGCTCTGGCAATACATCAAGATGCTGG 240
Db 181 ATCCTCCACTTACCTGGCTGTCCCTCGTACGCTCTGGCAATACATCAAGATGCTGG 240

QY 241 ATCCCTGTGAGCCYACCGTGCCTGGAAGTCCGCTGCGCGCCACCGCCTCTCTCCGC 300
Db 241 ATCCCTGTGAGCCYACCGTGCCTGGAAGTCCGCTGCGCGCCACCGCCTCTCTCCGC 300

QY 301 ACGCAGTGGATATGATGTTGGGCGGCGCACCTATGCTACGCTCTCTACGTAGGAGAC 360
Db 301 ACGCAGTGGATATGATGTTGGGCGGCGCACCTATGCTACGCTCTCTACGTAGGAGAC 360

QY 361 CTTTGTGAGCGCTATTCTTGTGCGGAGGGTCTCATGAGACATCGCCAGCATTTGG 420
Db 361 CTTTGTGAGCGCTATTCTTGTGCGGAGGGTCTCATGAGACATCGCCAGCATTTGG 420

QY 421 ACTGTCAGGACTGCAACTGTTCCATC 447
Db 421 ACTGTCAGGACTGCAACTGTTCCATC 447

RESULT 5
US-09-851-138-51
; Sequence 51, Application US/09851138
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
```

```
;
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-851-138-51

Query Match 99.7%; Score 445.8; DB 36; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTGGCTCTTCTCTATCTCTCTG 60
Db 1 GACGGAATTAATTCGCAACAGGGAATTTACCTGGTGGCTCTTCTCTATCTCTCTG 60

QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCGGGCTGGAGTACCGTAATGCTCCGGA 120
Db 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCGGGCTGGAGTACCGTAATGCTCCGGA 120

QY 121 CTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCGCGGGATATT 180
Db 121 CTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCGCGGGATATT 180

QY 181 ATCCTCCACTTACCTGGCTGTCCCTCGTACGCTCTGGCAATACATCAAGATGCTGG 240
Db 181 ATCCTCCACTTACCTGGCTGTCCCTCGTACGCTCTGGCAATACATCAAGATGCTGG 240

QY 241 ATCCCTGTGAGCCYACCGTGCCTGGAAGTCCGCTGCGCGCCACCGCCTCTCTCCGC 300
Db 241 ATCCCTGTGAGCCYACCGTGCCTGGAAGTCCGCTGCGCGCCACCGCCTCTCTCCGC 300

QY 301 ACGCAGTGGATATGATGTTGGGCGGCGCACCTATGCTACGCTCTCTACGTAGGAGAC 360
Db 301 ACGCAGTGGATATGATGTTGGGCGGCGCACCTATGCTACGCTCTCTACGTAGGAGAC 360

QY 361 CTTTGTGAGCGCTATTCTTGTGCGGAGGGTCTCATGAGACATCGCCAGCATTTGG 420
Db 361 CTTTGTGAGCGCTATTCTTGTGCGGAGGGTCTCATGAGACATCGCCAGCATTTGG 420

QY 421 ACTGTCAGGACTGCAACTGTTCCATC 447
Db 421 ACTGTCAGGACTGCAACTGTTCCATC 447
```



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RESULT 6
US-09-851-138B-51
; Sequence 51, Application US/09851138B
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; FILE REFERENCE: 2551-105
; CURRENT APPLICATION NUMBER: US/09/851,138B
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: EP 95870076.7
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 51
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-851-138B-51

Query Match          99.7%; Score 445.8; DB 36; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGCAACAGGGAATTTACCTGGTGTCTCTTCTATCTCTCTCTCTG 60
DB 1 GACGGAATTAATTTCGCAACAGGGAATTTACCTGGTGTCTCTTCTATCTCTCTCTCTG 60

QY 61 GCTTTGTTCTCATGCTTGTCTTACCCACAGCGGGCTGGAGTACCGTAATGCTCTCCGA 120
DB 61 GCTTTGTTCTCATGCTTGTCTTACCCACAGCGGGCTGGAGTACCGTAATGCTCTCCGA 120

QY 121 CTCTACATGTAATAACGACTGACGTAACGAGTATGCTGTATGAGCCCGGGGATATT 180
DB 121 CTCTACATGTAATAACGACTGACGTAACGAGTATGCTGTATGAGCCCGGGGATATT 180

QY 181 ATCTCTCACTTACCTGGCTGTGTCCTCGGTACGCTGCGGCAATACATCAAGATGCTGG 240
DB 181 ATCTCTCACTTACCTGGCTGTGTCCTCGGTACGCTGCGGCAATACATCAAGATGCTGG 240

QY 241 ATCCCTGTGAGCCYACCGTCCGCGTGAAGTCCGCGCCGCGCCACCGCTCTCTCCGC 300
DB 241 ATCCCTGTGAGCCYACCGTCCGCGTGAAGTCCGCGCCGCGCCACCGCTCTCTCCGC 300

QY 301 AGCAGCTGGATATGATGTGGGCGCGCACCCCTATGCTCAGCTCTCTACGTAGGAGAC 360
DB 301 AGCAGCTGGATATGATGTGGGCGCGCACCCCTATGCTCAGCTCTCTACGTAGGAGAC 360

QY 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGGTTCTCATGAGACATCGCCAGCATTTGG 420
DB 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGGTTCTCATGAGACATCGCCAGCATTTGG 420

QY 421 ACTGTCCAGGACTGCAACTGTTCCATC 447
DB 421 ACTGTCCAGGACTGCAACTGTTCCATC 447

RESULT 7
US-09-851-138C-51
; Sequence 51, Application US/09851138C
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; FILE REFERENCE: 2551-106
; CURRENT APPLICATION NUMBER: US/09/851,138C
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: EP 95870076.7
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 220
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-851-138C-51

Query Match          99.7%; Score 445.8; DB 36; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGCAACAGGGAATTTACCTGGTGTCTCTTCTATCTCTCTCTG 60
DB 1 GACGGAATTAATTTCGCAACAGGGAATTTACCTGGTGTCTTCTATCTCTCTCTCTG 60

QY 61 GCTTTGTTCTCATGCTTGTCTTACCCACAGCGGGCTGGAGTACCGTAATGCTCTCCGA 120
DB 61 GCTTTGTTCTCATGCTTGTCTTACCCACAGCGGGCTGGAGTACCGTAATGCTCTCCGA 120

QY 121 CTCTACATGTAATAACGACTGACGTAACGAGTATGCTGTATGAGCCCGGGGATATT 180
DB 121 CTCTACATGTAATAACGACTGACGTAACGAGTATGCTGTATGAGCCCGGGGATATT 180

QY 181 ATCTCTCACTTACCTGGCTGTGTCCTCGGTACGCTGCGGCAATACATCAAGATGCTGG 240
DB 181 ATCTCTCACTTACCTGGCTGTGTCCTCGGTACGCTGCGGCAATACATCAAGATGCTGG 240

QY 241 ATCCCTGTGAGCCYACCGTCCGCGTGAAGTCCGCGCCGCGCCACCGCTCTCTCCGC 300
DB 241 ATCCCTGTGAGCCYACCGTCCGCGTGAAGTCCGCGCCGCGCCACCGCTCTCTCCGC 300

QY 301 AGCAGCTGGATATGATGTGGGCGCGCACCCCTATGCTCAGCTCTCTACGTAGGAGAC 360
DB 301 AGCAGCTGGATATGATGTGGGCGCGCACCCCTATGCTCAGCTCTCTACGTAGGAGAC 360

QY 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGGTTCTCATGAGACATCGCCAGCATTTGG 420
DB 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGGTTCTCATGAGACATCGCCAGCATTTGG 420

QY 421 ACTGTCCAGGACTGCAACTGTTCCATC 447
DB 421 ACTGTCCAGGACTGCAACTGTTCCATC 447

RESULT 8
US-08-836-075B-220
; Sequence 220, Application US/08836075B
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; FILE REFERENCE: 2551-105
; CURRENT APPLICATION NUMBER: US/08/836,075B
; CURRENT FILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: EP 95870076.7
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 220
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-08-836-075B-220

Query Match          57.2%; Score 255.8; DB 14; Length 957;
Best Local Similarity 73.6%; Pred. No. 6e-61;
Matches 326; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGCAACAGGGAATTTACCTGGTGTCTCTTCTATCTCTCTCTG 60
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; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 51
; LENGTH: 447
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-851-138C-51

Query Match          99.7%; Score 445.8; DB 36; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGCAACAGGGAATTTACCTGGTGTCTCTTCTATCTCTCTCTG 60
DB 1 GACGGAATTAATTTCGCAACAGGGAATTTACCTGGTGTCTTCTATCTCTCTCTCTG 60

QY 61 GCTTTGTTCTCATGCTTGTCTTACCCACAGCGGGCTGGAGTACCGTAATGCTCTCCGA 120
DB 61 GCTTTGTTCTCATGCTTGTCTTACCCACAGCGGGCTGGAGTACCGTAATGCTCTCCGA 120

QY 121 CTCTACATGTAATAACGACTGACGTAACGAGTATGCTGTATGAGCCCGGGGATATT 180
DB 121 CTCTACATGTAATAACGACTGACGTAACGAGTATGCTGTATGAGCCCGGGGATATT 180

QY 181 ATCTCTCACTTACCTGGCTGTGTCCTCGGTACGCTGCGGCAATACATCAAGATGCTGG 240
DB 181 ATCTCTCACTTACCTGGCTGTGTCCTCGGTACGCTGCGGCAATACATCAAGATGCTGG 240

QY 241 ATCCCTGTGAGCCYACCGTCCGCGTGAAGTCCGCGCCGCGCCACCGCTCTCTCCGC 300
DB 241 ATCCCTGTGAGCCYACCGTCCGCGTGAAGTCCGCGCCGCGCCACCGCTCTCTCCGC 300

QY 301 AGCAGCTGGATATGATGTGGGCGCGCACCCCTATGCTCAGCTCTCTACGTAGGAGAC 360
DB 301 AGCAGCTGGATATGATGTGGGCGCGCACCCCTATGCTCAGCTCTCTACGTAGGAGAC 360

QY 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGGTTCTCATGAGACATCGCCAGCATTTGG 420
DB 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGGTTCTCATGAGACATCGCCAGCATTTGG 420

QY 421 ACTGTCCAGGACTGCAACTGTTCCATC 447
DB 421 ACTGTCCAGGACTGCAACTGTTCCATC 447
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RESULT 8
US-08-836-075B-220
; Sequence 220, Application US/08836075B
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; FILE REFERENCE: 2551-105
; CURRENT APPLICATION NUMBER: US/08/836,075B
; CURRENT FILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: EP 95870076.7
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 220
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-08-836-075B-220

Query Match          57.2%; Score 255.8; DB 14; Length 957;
Best Local Similarity 73.6%; Pred. No. 6e-61;
Matches 326; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGCAACAGGGAATTTACCTGGTGTCTTCTTCTATCTCTCTCTG 60
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Db
898 ACCGTCCAGTTGTGCAATTGCTC 920

RESULT 11

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US-09-851-138C-220
; Sequence 220, Application US/09851138C
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.
; FILE REFERENCE: 2551-106
; CURRENT APPLICATION NUMBER: US/09/851.138C
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: EP 95870076.7
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 220
; LENGTH: 957
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-851-138C-220

```

Query Match	57.2%	Score 255.8;	DB 36;	Length 957;
Best Local Similarity	73.6%	Pred. NO. 6e-61;		
Matches 326; Conservative	0;	Mismatches 117;	Indels 0;	Gaps 0;

Qy	1	GACGGAATTAATTTCCGCAACAGGGAAATTTA	CTGTTGCTCTTTCTCTATCTTCCCTCTCG	60
Db	478	GACGGAATAAACTTTGCAACAGGGAAATTTG	CCGGTTGCTCTTTTCTATCTTCCCTCTTT	537
Qy	61	GCTTTGTCTCATGCTTCTCTTACACCCACAG	CGGGCTGGAGTACGGTAATGCCTCCCGGA	120
Db	538	GCTCTCTTCTCATGCTTGTTTCCCGGAGCGG	GGCTTAGAGTACAGGAACACGCTCCGCG	597
Qy	121	CTCTACATGTTAACTAACGACTGCAAGTAA	CGGTAGTATCGTGTATGAGCCCGGGGATTT	180
Db	598	CTATACATACTTACCAACGACTGCTCTAAC	AGCAGCATCGTGTATGAGGCTGATAATGTC	657
Qy	181	ATCCTCCACATTAACCTGGCTGTCCCTCGGT	PACGCTCTGGCAATACATCAAGATGCTGG	240
Db	658	ATCTGCACATGCCCGGCTGTGTCCCTTGCA	CTCCGAGGGTAACAGGTCAAGGTGCTGG	717
Qy	241	ATCCCTGTGAGCCCVACCGTCCGCGGTGAAG	TGCGCCTGCGCCGCAACGCGCTCTCTCCGC	300
Db	718	ACGCCAGTAAACACGACAGTGGCTGTCAAA	CATCTGGCGCAGTCACCGCATCAATCCGC	777
Qy	301	ACGCACGTGGATATGATGGTGGGRCGGCGAC	CCCTTATGCTCAGCTCTCTACGTAGGACAC	360
Db	778	AGGCATGTGGAATTTGATGGTGGGTGCAGCC	ACGCTGTGTTTCAGCATCTCTATGTTGGAGAT	837
Qy	361	CTTTGTGGAGCGCTATTTCTTTGTGGGCAAG	GGGTTCTCATGGAGACATCGCCAGCATGG	420
Db	838	TTGTGGGGGCTGTTTTCTTTGTGGGCCAAG	GGTTTCATTTTCAGAGCTCGGCAACATTA	897
Qy	421	ACTGTCAGGACTGCAACTGTTTC	443	
Db	898	ACCGTCAGTTGTGCAATTGCTC	920	

RESULT 12

RESULT 12
US-08-836-075B-218
; Sequence 218, Application US/08836075B
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.
; FILE REFERENCE: 2551-105
; CURRENT APPLICATION NUMBER: US/08/836.075B
; CURRENT FILING DATE: 1997-04-21

```

; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: EP 95870076.7
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 957
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-08-836-075B-218

```

Query Match	56.4%	Score 252.2	DB 14	Length 957
Best Local Similarity	72.9%	Pred. No. 6.2e-60		
Matches 32;	Conservative 1;	Mismatches 119;	Indels 0;	Gaps 0;
Qy	1	GACGGAAATTAATTCGCAACAGGGAATTTACCTGGTTGCTCTTTCTCTATCTCTCTCTCTG 60		
Db	478	GACGGAAATTAATTCGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTCTCTCTG 537		
Qy	61	GCCTTGTTCATCTGCTTGTCTTACACCCACAGCGGGCTGGAGTAGACCTGAATGCTCTCGGA 120		
Db	538	GCCTTGTCTCTTGTCTTGGTCTGCTCTGCTGACGGGATTTGAATACCGGAATGTGCTGCG 597		
Qy	121	CTCTACATGGTAATTAACGACTGCGAGTAACCGTAGTATCGTGTATGAGCGCGGGATATT 180		
Db	598	CTCTACGTGCTACCAACGACTGCTCTAAACCGCAGTATCGTGTATGAGGCCCTCGAAGTC 657		
Qy	181	ATCTCTCACTTAACCTGCTGTGCCCTGCGTAGCTCTGGCAATAATCAAGATGCTGG 240		
Db	658	ATCTTGCACTTGCCAGGTTGTGTGCCCTGCGTTCAATCAGGCAACTCTCTGCAATGCTGG 717		
Qy	241	ATCCCTGTAGCCCYACCGTCCGCGTGAAGTCCGCCCTGCGCGGCCACCGGCTCTCTCCGC 300		
Db	718	ATTCCGCTGGCCACCAACAGTGGGGGGTTAAGTAGCGTGGCGCGAACCACTGCATCGATCCGC 777		
Qy	301	ACGCACGTGGATATGATGTTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAGGAGAC 360		
Db	778	AGTCATGTGGATCTGCTGTGGGAGCTGCTACGTTGTGCTCCGCGCTGTATGTTGGCGAT 837		
Qy	361	CTTTTGTGGACGGCTATTTCTTGTGTGGCAGGGGTTCTCATGGAGACATCGCCAGCATTTGG 420		
Db	838	ATGTGTGGACCGCTCTCTTGTGTGGGACAGGCTTTCACCTTCAGACCTCGTCAGCACAAAC 897		
Qy	421	ACTGTCCAGCACTGCAACTGTTTC 443		
Db	898	ACGGTGCAGACCTGCAATTGCTC 920		

RESULT 13

```

US-09-374-494A-218
; Sequence 218, Application US/09374494A
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.
; FILE REFERENCE: 46 USdvl
; CURRENT APPLICATION NUMBER: US/09/374,494A
; CURRENT FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: EP 95870076.7
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 957
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-374-494A-218

```

Query Match	56.4%	Score 252.2;	DB 21;	Length 957;
Best Local Similarity	72.9%	Pred. No. 6.2e-60;		

Matches 323; Conservative 1; Mismatches 119; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTTCGCAACAGGGAATTTTACCTGGTTGCTCTTCTCTATCTCTCTCTCTG 60
Db 478 GACGGAATTAATTTTCGCAACAGGGAATTTTACCGGTTGCTCTTCTCTATCTCTCTCTG 537
QY 61 GCTTTGTTCTCATGCTTCTCTTACACCAAGCCGGCTGGAGTACCGTAATGCTCCGGA 120
Db 538 GCTTTGTTCTCTCTCTGTTGCTCTCTGCTGAGGATTAATACCGGAATGCTGGC 597
QY 121 CTCTACATGTAATTAACGACTGAGTAACAGGTAGTATCTGTATGAGCCGGGGATATT 180
Db 598 CTCTACATGTAATTAACGACTGAGTAACAGGTAGTATCTGTATGAGCCGGGGATATT 657
QY 181 ATCCCTCCACTTACCTGGCTGTGCTCCCTGGTACGCTCTGGCAATACATCAAGATGCTGG 240
Db 658 ATCTTGACCTTCCAGGTTGTGTGCCCTGCTGCTCAATCAGGCAACTCTCTCGAATGCTGG 717
QY 241 ATCCCTGTGAGCCYACCGTGCCTGCTGAGTGCCTGCGCCGACCGCTCTCTCCGC 300
Db 718 ATCCGGTGGCAACACAGTGGCGGTAAAGTACGCTGGCGGACCACTGCATCGATCCGC 777
QY 301 ACGCAGTGGATATGATGTTGGGCGGCGCACCTATGCTAGCTCTCTACGTAGGAGAC 360
Db 778 AGTCATGTTGATCTCTGCTGGTGGAGCTGTACGTTGTGCTCCGCGCTGTATGTTGGCGAT 837
QY 361 CTCTGTGAGCGCTATTTCTTGTGGGAGGGTTCTCATGGAGACATCGCCAGCATGG 420
Db 838 ATGTTGTGAGCGCTCTTCTTGTGGGACAGGCTTTCACCTTCAGACCTCGTCAGCAAC 897
QY 421 ACTGTCAGGACTGCAACTGTTTC 443
Db 898 ACGGTGCAGACCTGCAATTGCTC 920

RESULT 14
US-09-851-138B-218
; Sequence 218, Application US/09851138B
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.
; FILE REFERENCE: 2551-106
; CURRENT APPLICATION NUMBER: US/09/851,138B
; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 1994-10-21
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 957
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-851-138B-218

Query Match 56.4%; Score 252.2; DB 36; Length 957;
Best Local Similarity 72.9%; Pred. No. 6.2e-60;
Matches 323; Conservative 1; Mismatches 119; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTTCGCAACAGGGAATTTTACCTGGTTGCTCTTCTCTATCTCTCTCTG 60
Db 478 GACGGAATTAATTTTCGCAACAGGGAATTTTACCGGTTGCTCTTCTCTATCTCTCTCTG 537
QY 61 GCTTTGTTCTCATGCTTCTCTTACACCAAGCCGGCTGGAGTACCGTAATGCTCCGGA 120
Db 538 GCTTTGTTCTCTCTCTGTTGCTCTCTGCTGAGGATTAATACCGGATGCTCTCTCTGCTT 537
QY 61 GCTTTGTTCTCATGCTTCTCTTACACCAAGCCGGCTGGAGTACCGTAATGCTCCGGA 120
Db 538 GCTTTGTTCTCTCTCTGTTGCTCTCTGCTGAGGATTAATACCGGAATGCTGCTGGC 597
QY 121 CTCTACATGTAATTAACGACTGAGTAACAGGTAGTATCTGTATGAGCCGGGGATATT 180
Db 598 CTCTACATGTAATTAACGACTGAGTAACAGGTAGTATCTGTATGAGCCGGGGATATT 657

QY 181 ATCCCTCCACTTACCTGGCTGTGCTCCCTGGTACGCTCTGGCAATACATCAAGATGCTGG 240
Db 658 ATCTTGACCTTCCAGGTTGTGTGCCCTGCTGCTCAATCAGGCAACTCTCTCGAATGCTGG 717
QY 241 ATCCCTGTGAGCCYACCGTGCCTGCTGAGTGCCTGCGCCGACCGCTCTCTCCGC 300
Db 718 ATCCGGTGGCAACACAGTGGCGGTAAAGTACGCTGGCGGACCACTGCATCGATCCGC 777
QY 301 ACGCAGTGGATATGATGTTGGGCGGCGCACCTATGCTAGCTCTCTACGTAGGAGAC 360
Db 778 AGTCATGTTGATCTCTGCTGGTGGAGCTGTACGTTGTGCTCCGCGCTGTATGTTGGCGAT 837
QY 361 CTCTGTGAGCGCTATTTCTTGTGGGAGGGTTCTCATGGAGACATCGCCAGCATGG 420
Db 838 ATGTTGTGAGCGCTCTTCTTGTGGGACAGGCTTTCACCTTCAGACCTCGTCAGCAAC 897
QY 421 ACTGTCAGGACTGCAACTGTTTC 443
Db 898 ACGGTGCAGACCTGCAATTGCTC 920

RESULT 15
US-09-851-138C-218
; Sequence 218, Application US/09851138C
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.
; FILE REFERENCE: 2551-106
; CURRENT APPLICATION NUMBER: US/09/851,138C
; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 2001-05-09
; PRIOR FILING DATE: 1994-10-21
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 957
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-851-138C-218

Query Match 56.4%; Score 252.2; DB 36; Length 957;
Best Local Similarity 72.9%; Pred. No. 6.2e-60;
Matches 323; Conservative 1; Mismatches 119; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTTCGCAACAGGGAATTTTACCTGGTTGCTCTTCTCTATCTCTCTCTG 60
Db 478 GACGGAATTAATTTTCGCAACAGGGAATTTTACCGGTTGCTCTTCTCTATCTCTCTCTG 537
QY 61 GCTTTGTTCTCATGCTTCTCTTACACCAAGCCGGCTGGAGTACCGTAATGCTCCGGA 120
Db 538 GCTTTGTTCTCTCTCTGTTGCTCTCTGCTGAGGATTAATACCGGAATGCTGCTGGC 597
QY 121 CTCTACATGTAATTAACGACTGAGTAACAGGTAGTATCTGTATGAGCCGGGGATATT 180
Db 598 CTCTACATGTAATTAACGACTGAGTAACAGGTAGTATCTGTATGAGCCGGGGATATT 657
QY 181 ATCCCTCCACTTACCTGGCTGTGCTCCCTGGTACGCTCTGGCAATACATCAAGATGCTGG 240
Db 658 ATCTTGACCTTCCAGGTTGTGTGCCCTGCTGCTCAATCAGGCAACTCTCTCGAATGCTGG 717
QY 241 ATCCCTGTGAGCCYACCGTGCCTGCTGAGTGCCTGCGCCGACCGCTCTCTCCGC 300
Db 718 ATCCGGTGGCAACACAGTGGCGGTAAAGTACGCTGGCGGACCACTGCATCGATCCGC 777
QY 301 ACGCAGTGGATATGATGTTGGGCGGCGCACCTATGCTAGCTCTCTACGTAGGAGAC 360
Db 778 AGTCATGTTGATCTCTGCTGGTGGAGCTGTACGTTGTGCTCCGCGCTGTATGTTGGCGAT 837
QY 361 CTCTGTGAGCGCTATTTCTTGTGGGAGGGTTCTCATGGAGACATCGCCAGCATGG 420

Db 838 ATGTGTGGAGCCGTCTTCTTGGTGGACAGGCTTTCACCTTCAGACCTCGTCAGACAAC 897

Qy 421 ACTGTCCAGGACTGCAACTGTTTC 443

Db 898 ACGGTGCAGACCTGCAATTGCTC 920

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-851-138C-51
Perfect score: 447
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Scoring table: IDENTITY_NUC
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Searched: 4390206 seqs, 2959870667 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	445.8	99.7	447	2 AAT27962	Aat27962 Hepatitis
2	236.2	52.8	540	2 AAT278031	Aag78031 Hepatitis
3	236.2	52.8	541	2 AAT278029	Aag78029 Hepatitis
4	234.6	52.5	541	2 AAT278033	Aag78033 Hepatitis
5	234.6	52.5	541	2 AAT278036	Aag78036 Hepatitis
6	234.6	52.5	541	2 AAT278032	Aag78032 Hepatitis
7	233	52.1	541	2 AAT278030	Aag78030 Hepatitis
8	233	52.1	541	2 AAT278034	Aag78034 Hepatitis
9	233	52.1	541	2 AAT278035	Aag78035 Hepatitis
10	233	52.1	630	2 AAT12965	Aat12965 HCV E1 co
11	233	52.1	630	6 AAL48929	Aal48929 Hepatitis
12	233	52.1	630	10 ADD5537	Add5537 Hepatitis
13	233	52.1	630	12 ADP71119	Adp71119 HCV DNA e
14	221.4	49.5	1249	2 AAT27858	Aat27858 HCV J1 NS
15	219.4	49.1	565	2 AAT27858	Aat27858 HCV J1 NS
16	217.4	48.6	579	2 AAT278104	Aag78104 Hepatitis
17	216.2	48.4	580	2 AAT27852	Aaz07852 HCV E dom
18	215.8	48.3	574	2 AAT278081	Aag78081 Hepatitis
19	215.8	48.3	579	2 AAT278106	Aag78106 Hepatitis
20	215.8	48.3	579	2 AAT278103	Aag78103 Hepatitis

21	209.8	46.9	447	2 AAT27956	Aat27956 Hepatitis
22	209	46.8	447	2 AAT27952	Aat27952 Hepatitis
23	208.6	46.7	447	2 AAT27955	Aat27955 Hepatitis
24	206.6	46.2	579	2 AAT278102	Aag78102 Hepatitis
25	206.2	46.1	579	2 AAT278109	Aag78109 Hepatitis
26	205	45.9	579	2 AAT278101	Aag78101 Hepatitis
27	204.6	45.8	574	2 AAT278080	Aag78080 Hepatitis
28	204.2	45.7	1270	2 AAT278080	Aag78080 Hepatitis
29	204.2	45.7	1562	2 AAT278080	Aag78080 Hepatitis
30	204.2	45.7	1562	2 AAT278080	Aag78080 Hepatitis
31	204.2	45.7	2116	8 AAL55222	Aal55222 Plasmid P
32	204.2	45.7	2116	8 AAL55222	Aal55222 Plasmid P
33	203	45.4	579	2 AAT278114	Aag78114 Hepatitis
34	203	45.4	579	2 AAT278108	Aag78108 Hepatitis
35	201.4	45.1	579	2 AAT278113	Aag78113 Hepatitis
36	201.4	45.1	579	2 AAT278093	Aag78093 Hepatitis
37	201	45.0	447	2 AAT27951	Aat27951 Hepatitis
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40	199.4	44.6	742	2 AAT27951	Aat27951 Hepatitis
41	198.2	44.3	447	2 AAT27954	Aat27954 Hepatitis
42	197.8	44.3	447	2 AAT27953	Aat27953 Hepatitis
43	196.2	43.9	577	2 AAT35082	Aag35082 HCV envel
44	196.2	43.9	633	2 AAT12706	Aat12706 HCV E1 co
45	196.2	43.9	633	6 AAL48915	Aal48915 Hepatitis

ALIGNMENTS

RESULT 1
AAT27962
ID AAT27962 standard; DNA; 447 BP.
XX
AC AAT27962;
DT 11-MAR-1997 (first entry)
XX
DE Hepatitis C virus type 10a isolate NN98 bases 478-925.
XX
KW Hepatitis C virus; subtype; polymerase chain reaction; amplification;
KW PCR; primer; probe; antibody; infection; ss.
XX
OS Hepatitis C virus.
XX
PN WO9613590-A2.
XX
PD 09-MAY-1996.
XX
PF 23-OCT-1995; 95WO-EP004155.
XX
PR 21-OCT-1994; 94EP-00870166.
PR 28-JUN-1995; 95EP-00870076.
XX
(INNO-) INNOGENETICS NV.
XX
PI Maertens G, Stuyver L;
XX
DR WPI; 1996-251460/25.
XX
P-PSDB; AAR96551.
XX
Hepatitis C virus polynucleic acid unique to unidentified sub-type -
PT used to develop probes and primers for new subtypes and vaccines to
prevent and treat infection.
XX
PS Claim 6; Fig 3; 150pp; English.
XX
The sequences AAT27937-727999 represent novel sequences isolated from
CC hepatitis C virus subtypes different from subtypes 1a-c, 2a-d, 3a-f, 4a-
CC j, 5a and 6a. They esp. from the novel subtypes 1d-f, 2e-i, 2k, 2l, 3g,
CC 4k-m, 7a-c or types 9, 10 or 11. The sequences corresp. to the 5'
untranslated region (UR), the Core/E1, NS4 or NS5B regions of the genome.
CC This sequence represents nucleotides 478-925 from the HCV type 10a

RESULT 3
 AAQ78029
 ID AAQ78029 standard; cdNA; 541 BP.
 XX
 AC AAQ78029;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-JUL-1995 (first entry)
 XX
 DE Hepatitis C virus Core/E1 region.
 XX
 KW Hepatitis C virus; HCV; primer; probe; detection; diagnosis;
 KW classification; immunisation; prophylaxis; serotyping; ss.
 XX
 OS Hepatitis C virus type 3a.
 XX
 FH Key Location/Qualifiers
 FT CDS 2..541
 FT /*tag= a
 FT /product= "Core/E1 polypeptide."
 XX
 PN WO9425601-A2.
 XX
 PD 10-NOV-1994.
 XX
 PF 27-APR-1994; 94WO-EP001323.
 XX
 PR 27-APR-1993; 93EP-00401099.
 PR 05-AUG-1993; 93EP-00402019.
 XX
 PA (INNO-) INNOGENETICS NV SA.
 XX
 PI Maertens G, Stuyver L;
 XX
 DR WPI; 1994-358277/44.
 DR P-PSDB; AAR63277.
 XX
 New polynucleotide sequences from hepatitis C virus - and related
 PT vectors, polypeptide(s) and antibodies, useful for immunisation,
 PT treatment, diagnosis and typing of HCV isolates.
 XX
 PS Claim 2; Page 103-104; 404pp; English.
 XX
 CC Compositions comprising at least 5, and pref. 8 or more contiguous
 CC nucleotides selected from an HCV type 3 genomic sequence, more
 CC particularly (i) the region spanning positions 417-957 of the Core/E1
 CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of
 CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-
 CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning
 CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype
 CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to
 CC amplify nucleic acid from an isolate belonging to a specific genotype, or
 CC as a probe for specific detection/classification of nucleic acid.
 CC Polypeptides encoded by the nucleotides in such compositions may be used
 CC for immunisation against HCV, for the detection of antibodies directed
 CC against HCV and for serotyping. This sequence corresponds to the Core/E1
 CC region of HCV subtype 3a and is taken from a clone designated HD10-2-5.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 541 BP; 104 A; 153 C; 145 G; 139 T; 0 U; 0 Other;
 Query Match 52.8%; Score 236.2; DB 2; Length 541;
 Best Local Similarity 70.7%; Pred. No. 1.3e-63;
 Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps 0;
 1 GACGGAATTAATTCGCAACAGGAATTTACTGGTGTCTTCTCTATCTCTCTCG 60
 62 GACGGGATAAATTCGCAACAGGAATTTCTCCGGTGTCTCTTCTATCTCTCTT 121
 61 GCTTTGTCTCTATGCTTGTACACCCAGCGGGCTGGATACCGTAATCCTCCGGA 120

Db 122 GCTCTGTTCTTCTGCTTAATCCATCCAGCAGCTAGTCTAGAGTGGCGGNACAGCTCTGGC 181
 QY 121 CTCTACATGGTAACCTAACGACTGCGAGTAACGGTAGTATCGTGTATGAGCGCGGGATATT 180
 Db 182 CTCTATGCTCTTACCAACGACTGTTCCCAATAGCAGTATTGTGTATGAGCGCGGATGACGTT 241
 QY 181 ATCCTCCCACTTACCTGGCTGTGCTCCCTGCGTACGCTCTGGCAATACATCAAGATGCTCG 240
 Db 242 ATTCTGCACACACCGGCTGTGTACCTTGTGTTCAGGACGGTAATACATCTGGGCTCTGG 301
 QY 241 ATCCCTGTGAGCCYACCGTTCGCCGTGAAGTTCGCCCTGCGCGCCGCCACCCCTCTCTCCGC 300
 Db 302 ACCCCAGTGACACCTACAGTGCAGTACGTCGGAGCAACCAACCGCTTCGATACGC 361
 QY 301 AGCAGCTGGATATGATGTTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAGAGAC 360
 Db 362 AGGCATGTAGACATGTGTGGGCGCGCCACGATGTCTCTGCTCTCTACGTGGGTGAT 421
 QY 361 CTTTGTGGAGCGCTATTCTTGTGGGCGAGGGTTCATGAGAGACATCGCCAGCATTCG 420
 Db 422 ATGTGTGGGCGGCTCTTCTCTGTGGACAAGCCCTTCAGCTTCAGACCTCTGCGCCATCA 481
 QY 421 ACTGTCCAGGACTGCAACTGTTTC 443
 Db 482 ACGGTCCAGACCTGTAACTGCTC 504
 RESULT 4
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 ID AAQ78033 standard; cdNA; 541 BP.
 XX
 AC AAQ78033;
 XX
 DT 25-MAR-2003 (revised)
 DT 01-AUG-1995 (first entry)
 XX
 DE Hepatitis C virus Core/E1 region.
 XX
 KW Hepatitis C virus; HCV; primer; probe; detection; diagnosis;
 KW classification; immunisation; prophylaxis; serotyping; ss.
 XX
 OS Hepatitis C virus type 3a.
 XX
 FH Key Location/Qualifiers
 FT CDS 2..541
 FT /*tag= a
 FT /product= "Core/E1 polypeptide."
 XX
 PN WO9425601-A2.
 XX
 PD 10-NOV-1994.
 XX
 PF 27-APR-1994; 94WO-EP001323.
 XX
 PR 27-APR-1993; 93EP-00401099.
 PR 05-AUG-1993; 93EP-00402019.
 XX
 PA (INNO-) INNOGENETICS NV SA.
 XX
 PI Maertens G, Stuyver L;
 XX
 DR WPI; 1994-358277/44.
 DR P-PSDB; AAR63281.
 XX
 New polynucleotide sequences from hepatitis C virus - and related
 PT vectors, polypeptide(s) and antibodies, useful for immunisation,
 PT treatment, diagnosis and typing of HCV isolates.
 XX
 PS Claim 2; Page 111-112; 404pp; English.
 XX
 CC Compositions comprising at least 5, and pref. 8 or more contiguous
 CC nucleotides selected from an HCV type 3 genomic sequence, more
 CC particularly (i) the region spanning positions 417-957 of the Core/E1

CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of
 CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-
 CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning
 CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype
 CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to
 CC amplify nucleic acid from an isolate belonging to a specific genotype, or
 CC as a probe for specific detection/classification of nucleic acid.
 CC Polypeptides encoded by the nucleotides in such compositions may be used
 CC for immunisation against HCV, for the detection of antibodies directed
 CC against HCV and for serotyping. This sequence corresponds to the Core/E1
 CC region of HCV subtype 3a and is taken from a clone designated BR36-9-20.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 541 BP; 106 A; 154 C; 142 G; 139 T; 0 U; 0 Other;

Query Match 52.5%; Score 234.6; DB 2; Length 541;

Best Local Similarity 70.4%; Pred. No. 4.1e-63;
 Matches 312; Conservative 1; Mismatches 130; Indels 0; Gaps 0;

QY 1 GACGGATTAATTTCCGAACAGGGAATTTACCTGGTGTCTTTCTCTATCTCTCTCTG 60
 Db GACGGGATAAATTTCCGAACAGGGAATTTGCCGGTGTCTCTTTCTATTTCTCTCTT 121
 QY 61 GCTTTGTCTCATGCTTGCTTTACACCCAGCCGGCTGGAGTACCGTAATCGCTCCGGA 120
 Db 122 GCTCTGTCTCTTAAATTCATCCAGCAGTGTCTAGAGTGGCGGAATACGTCCTGGC 181
 QY 121 CTCTCATGTGTAATTAACGACTGCTTCCATAGCAGTATTTGTACGAGCCGGAATTT 180
 Db 182 CTCTATGTCTTACCAACGACTGTTCCATAGCAGTATTTGTACGAGCCGGAATTT 241
 QY 181 ATCTCCACTTACCTGGCTGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 Db 242 ATTCTGTCACACCCGGCTGTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
 QY 241 ATCTCTGTGAGCCVACCGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGG 300
 Db 302 ACCCCAGTGACACCTACAGTGGCAGTCAAGTACGTCGGAGCAACACCCTTCGATACGC 361
 QY 301 AGCAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Db 362 AGTCATGTGGACCTGTGTAGTGGCGGCCAGATGTCTCTGCTCTCTGCTCTCTGCTGCT 421
 QY 361 CTTTGTGGAGCGCTATTTCTCTGCGGAGCGGGTCTCATGAGACATCGCCAGCATGG 420
 Db 422 ATGTGTGGGGCTGTCTTCTCTGCGGACAAAGCTTTCAGCTTCAGACCTCGTGTGTCATCA 481
 QY 421 ACTGTCCAGGACTGCAACTGTTC 443
 Db 482 ACGGTCCAGACCTGTAACTGTCTC 504

RESULT 5

AAQ78036
 ID AAQ78036 standard; cdna; 541 BP.

AC AAQ78036;

DT 25-MAR-2003 (revised)
 DT 01-AUG-1995 (first entry)

XX Hepatitis C virus Core/E1 region.

XX Hepatitis C virus; HCV; primer; probe; detection; diagnosis;
 KW classification; immunisation; prophylaxis; serotyping; ss.

OS Hepatitis C virus type 3a.

XX Key Location/Qualifiers
 FH 2. 541
 FT CDS /tag= a
 FT /product= "Core/E1 polypeptide."

XX

PN WO9425601-A2.
 XX 10-NOV-1994.
 PD
 XX 27-APR-1994; 94WO-EP001323.
 PF
 XX 27-APR-1993; 93EP-00401099.
 PR
 XX 05-AUG-1993; 93EP-00402019.
 PR
 XX (INNO-) INNOGENETICS NV SA.
 PA
 XX Maertens G, Stuyver L;
 PI
 XX WPI; 1994-358277/44.
 DR
 XX P-PSDB; AAR63284.
 DR
 XX New polynucleotide sequences from hepatitis C virus - and related
 PT vectors, polypeptide(s) and antibodies, useful for immunisation,
 PT treatment, diagnosis and typing of HCV isolates.
 XX
 PS Claim 2; Page 117-118; 404pp; English.
 XX
 CC Compositions comprising at least 5, and pref. 8 or more contiguous
 CC nucleotides selected from an HCV type 3 genomic sequence, more
 CC particularly (i) the region spanning positions 417-957 of the Core/E1
 CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of
 CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-
 CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning
 CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype
 CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to
 CC amplify nucleic acid from an isolate belonging to a specific genotype, or
 CC as a probe for specific detection/classification of nucleic acid.
 CC Polypeptides encoded by the nucleotides in such compositions may be used
 CC for immunisation against HCV, for the detection of antibodies directed
 CC against HCV and for serotyping. This sequence corresponds to the Core/E1
 CC region of HCV subtype 3a and is taken from a clone designated BR33-1-20.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 541 BP; 100 A; 154 C; 148 G; 139 T; 0 U; 0 Other;

Query Match 52.5%; Score 234.6; DB 2; Length 541;
 Best Local Similarity 70.4%; Pred. No. 4.1e-63;

Matches 312; Conservative 1; Mismatches 130; Indels 0; Gaps 0;

QY 1 GACGGATTAATTTCCGAACAGGGAATTTACCTGGTGTCTTTCTCTATCTCTCTCTG 60
 Db 62 GACGGGATAAATTTCCGAACAGGGAATTTGCCGGTGTCTCTTTCTATTTCTCTCTT 121
 QY 61 GCTTTGTCTCATGCTTGCTTACCCAGCCGGCTGGAGTACCGTAATCGCTCCGGA 120
 Db 122 GCTCTGTCTCTTAAATTCATCCAGCAGTGTCTAGAGTGGCGGAATACGTCCTGGC 181
 QY 121 CTCTCATGTGTAATTAACGACTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 Db 182 CTCTATGTCTTACCAACGACTGTTCCATAGTATGATGATGATGATGATGATGATGATG 241
 QY 181 ATCTCCACTTACCTGGCTGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 Db 242 ATTCTGTCACGCGCGCTGTGTAGTGGCGGCCAGATGTCTCTGCTCTCTGCTCTCTGCT 301
 QY 241 ATCTCTGTGAGCCVACCGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGG 300
 Db 302 ACCCCAGTAAACCTACAGTGGCAGTCAAGTACGTCGGAGCAACACCCTTCGATACGC 361
 QY 301 AGCAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Db 362 AGTCATGTGGACCTGTGTAGTGGCGGCCAGATGTCTCTGCTCTCTGCTCTCTGCTGCT 421
 QY 361 CTTTGTGGAGCGCTATTTCTCTGCGGAGCGGGTCTCATGAGACATCGCCAGCATGG 420
 Db 422 ATGTGTGGGGCTGTCTTCTCTGCGGACAAAGCTTTCAGCTTCAGACCTCGTGTGTCATCA 481
 QY 421 ACTGTCCAGGACTGCAACTGTTC 443

CC nucleotides selected from an HCV type 3 genomic sequence, more
 CC particularly (i) the region spanning positions 417-957 of the Core/E1
 CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of
 CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-
 CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype
 CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to
 CC amplify nucleic acid from an isolate belonging to a specific genotype, or
 CC as a probe for specific detection/classification of nucleic acid.
 CC Polypeptides encoded by the nucleotides in such compositions may be used
 CC for immunisation against HCV, for the detection of antibodies directed
 CC against HCV and for serotyping. This sequence corresponds to the Core/E1
 CC region of HCV subtype 3a and is taken from a clone designated HD10-2-14.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 541 BP; 106 A; 154 C; 143 G; 138 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 2; Length 541;

Best Local Similarity 70.2%; Pred. No. 1.3e-62;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAAATTAATTCGCAACAGGGAATTTACCTGGTGTCTTTCTCTATCTTCTCTCTG 60

DB 62 GACGGGATAAATTTGCAACAGGGAATTTGCCGGTGTCTTTCTATCTTCTCTCT 121

QY 61 GCTTTGTCTCATGCTTGTACACCCAGCCGGCTGGAGTACGTAATGCTCCGGA 120

DB 122 GCTCTGTCTTCTTAAATCCATCCAGCAGTAGTCTAGAGTGGGGAACACGCTGCG 181

QY 121 CTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCCGGGATATT 180

DB 182 CTCTATGCTCTTACCAACGACTTCTCCATAGCAGTATTGTGTATGAGCCGATGACGTT 241

QY 181 ATCTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCCGGGATATT 240

DB 242 ATCTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCCGGGATATT 301

QY 241 ATCTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCCGGGATATT 300

DB 302 ACCCAAGTACACCTTACAGTGGGAGTACGTCAGTGGGAGCAACACCGCTTCCGATACGC 361

QY 301 ACACGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

DB 362 AGGCATGTAGACATATTGTTGGGCGCGCCACAAATGCTCTGCTCTCTACGTGGGTGAT 421

QY 361 CTCTTGGGAGCGTATTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420

DB 422 ATGTGTGGGCGCTTCTCTCTGTGGGCAAGCCCTTACGTTTCAGACCTCTCGTCCGATCAA 481

QY 421 ACTGTCCAGGACTGCAACTGTTC 443

DB 482 ACGGTCCAGACCTGTAACTGCTC 504

RESULT 8

AAQ78034

ID AAQ78034 standard; cdna; 541 BP.

XX

AC AAQ78034;

XX

DT 25-MAR-2003 (revised)

DT 01-AUG-1995 (first entry)

XX

DE Hepatitis C virus Core/E1 region.

XX

KW Hepatitis C virus; HCV; primer; probe; detection; diagnosis;

KW classification; immunisation; prophylaxis; serotyping; ss.

XX

OS Hepatitis C virus type 3a.

XX

PH Key Location/Qualifiers

FT CDS 2..541

FT /*tag= a

/product= "Core/E1 polypeptide."

WO9425601-A2.

10-NOV-1994.

27-APR-1994; 94WO-BP001323.

27-APR-1993; 93EP-00401099.

05-AUG-1993; 93EP-00402019.

(INNO-) INNOGENETICS NV SA.

Maertens G, Stuyver L;

WPI: 1994-358277/44.

P-PSDB; AAR63282.

New polynucleotide sequences from hepatitis C virus - and related
 vectors, polypeptide(s) and antibodies, useful for immunisation,
 treatment, diagnosis and typing of HCV isolates.

Claim 2; Page 113-114; 404pp; English.

Compositions comprising at least 5, and pref. 8 or more contiguous
 nucleotides selected from an HCV type 3 genomic sequence, more
 particularly (i) the region spanning positions 417-957 of the Core/E1
 region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of
 the NS3 region of HCV type 3; (iii) the region spanning positions 4892-
 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning
 positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype
 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to
 amplify nucleic acid from an isolate belonging to a specific genotype, or
 as a probe for specific detection/classification of nucleic acid.
 Polypeptides encoded by the nucleotides in such compositions may be used
 for immunisation against HCV, for the detection of antibodies directed
 against HCV and for serotyping. This sequence corresponds to the Core/E1
 region of HCV subtype 3a and is taken from a clone designated BR33-1-10.
 (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 541 BP; 100 A; 157 C; 148 G; 136 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 2; Length 541;

Best Local Similarity 70.2%; Pred. No. 1.3e-62;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAAATTAATTCGCAACAGGGAATTTACCTGGTGTCTTTCTCTATCTTCTCTG 60

DB 62 GACGGGATAAATTTGCAACAGGGAATTTGCCGGTGTCTTTCTATCTTCTCTT 121

QY 61 GCTTTGTCTCATGCTTGTCCCTGCTGAGTACCCAGCCGGCTGGAGTACCGTAATGCTCCGGA 120

DB 122 GCTCTGTCTTCTTAAATCCATCCAGCAGCTGGTCTAGAGTGGCGGATAGCTGCG 181

QY 121 CTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCCGGGATATT 180

DB 182 CTCTATGCTCTTACCAACGACTGTTCCAATAGTAGTATTGTGTATGAGCCGATGACGTT 241

QY 181 ATCTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCCGATGACGTT 240

DB 242 ATCTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCCGATGACGTT 301

QY 241 ATCTCTACATGTAATTAACGACTGACGTAACGGTAGTATCGTGTATGAGCCGATGACGTT 300

DB 302 ACCCAAGTACACCTTACAGTGGGAGTACGTCAGTGGGAGCAACACCGCTTCCGATACGC 361

QY 301 ACACGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

DB 362 AGTCATGTGGACCTGTGTAGTAGGCGCGCCACGATGTGCTCTGCGCTTTTACGTGGGTGAT 421

QY 361 CTCTTGGGAGCGCTATTCTTGTGGGCGAGGGTCTTCATGGAGACATCGCCGAGATTGG 420

DB 422 ATGTGTGGGCGCTTCTCTCTGTGGGCAACGCTTACGTTTCAGACCCCGCGCATCAA 481

XX 15-JAN-2004 (first entry)
XX Hepatitis C virus E1/E2 protein coding sequence #5.
XX Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;
KW liver fibrosis; ds; gene.
XX Hepatitis C virus.
OS WO2003051912-A2.
XX 26-JUN-2003.
XX 18-DEC-2002; 2002WO-BF014480.
XX 18-DEC-2001; 2001US-00020510.
PR 16-OCT-2002; 2002US-0418358P.
XX (INNO-) INNOGENETICS NV.
PA Maertens G, Depla E, Bosman F;
PI WPI: 2003-541632/51.
DR P-PSDB; ADP55538.
XX New hepatitis C virus (HCV) vaccine composition, useful for reducing
PT liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.
PT Example 2; SEQ ID NO 29; 271pp; English.
PS The invention comprises an Hepatitis C virus (HCV) vaccine for reducing
XX liver disease. The vaccine of the invention comprises an HCV E1 or E2
CC protein as an antigen. The HCV vaccine is useful for reducing liver
CC disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The
CC present DNA sequence encodes an HCV E1/E2 protein.
XX Sequence 630 BP; 127 A; 175 C; 168 G; 160 T; 0 U; 0 Other;
SQ Query Match 52.1%; Score 233; DB 10; Length 630;
Best Local Similarity 70.2%; Pred. No. 1.4e-62;
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;
QY 1 GACGGAATTAATTCGACACAGGGAATTTACCTGGTGTCTTTCTCTATCTCTCTG 60
Db 124 GACGGGATAAATTCGACACAGGGAATTTGCGCGGTGCTCTTTCTATTTCTCTCTC 183
QY 61 GCTTGTCTCTATGCTGTGTACACCCAGCGGGCTGGAGTACCGTAATGCTCCGGA 120
Db 184 GCTCTGTCTCTGTCTTAATTCATCCAGCAGCTAGTCTAGAGTGGGGAATACGTTGGC 243
QY 121 CTCATCATGTAACACTACGACTGCAGTAACGGTAGTATGCTGTATGAGCGCGGATATT 180
Db 244 CTCATGTCTTACCAACAGCTGTTCATAGACGATTTGTGTACGAGCGCCATGACGTT 303
QY 181 ATCTCCACTTACCTGGCTGTGTCCCTCGGACGCTCTGGCAATACATCAAGATGCTGG 240
Db 304 ATTCTGCACACACCCGGCTGCATACCTTGTCTCAGGAGCGCAATACATCCACGTCG 363
QY 241 ATCCCTGTGAGCCYACCTGCGGTGAAGTGCCTGCGCGCCGACCGCTCTCTCGC 300
Db 364 ACCCCAGTGACACCTACAGTGGCAGTCAAGTAGCTCGGAGCAACCAACCGCTTCGATAC 423
QY 301 AGCCAGCTGTATGATGTGGGCGCGCCACCTATGCTCAGCTCTCTACGTAGGAGAC 360
Db 424 AGTCATGTGAGCACTATTATGTGGGCGCGCCACGATGTGCTCTCGCTCTACGTGGGTGAC 483
QY 361 CTTTGTGGAGCGCTATTTCTTGTGGGCGAGGGTTCTATGAGACATCCGACGATGG 420
Db 484 ATGTGTGGGGCTGTCTTCTCGTGGGCAAGCGCTTCACGTTCCAGACCTCGTCCCATCAA 543
QY 421 ACTGTCCAGGACTGCACCTGTTTC ||||| ||||| ||||| |||||

Db 544 ACGTCCAGACCTGTAACTGCTC 566
RESULT 13
ADP71119
ID ADP71119 standard; cDNA; 630 BP.
XX
AC ADP71119;
XX
DT 23-SEP-2004 (first entry)
XX
DE HCV DNA encoding E1 protein HCC162.
XX
KW Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
KW liver disease; liver fibrosis; ss; serum alanine aminotransferase level;
KW steatosis; anti-E2 immunoreactivity; vaccine.
XX
OS Hepatitis C virus; type 3a.
XX
PN US2004126395-A1.
XX
PD 01-JUL-2004.
XX
PF 18-DEC-2002; 2002US-00321798.
XX
PR 18-DEC-2001; 2001US-0453708P.
PR 16-OCT-2002; 2002US-0418358P.
XX
PA (MAER/) MAERTENS G.
PA (DEPL/) DEPLA E.
PA (BOSM/) BOSMAN F.
XX
PI Maertens G, Depla E, Bosman F;
XX WPI: 2004-499089/47.
DR P-PSDB; ADP71120.
XX
PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver
PT disease, serum alanine aminotransferase levels, steatosis, or anti-E2
PT immunoreactivity in the liver of a chronic HCV-infected mammal.
XX
PS Example 2; SEQ ID NO 29; 176pp; English.
XX
CC The invention relates to the use of a hepatitis C virus (HCV) vaccine
CC composition for reducing liver disease (such as liver fibrosis or its
CC progression), serum alanine aminotransferase (ALT) levels, steatosis, or
CC anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,
CC or for treating a chronic HCV-infected mammal. The liver disease is
CC reduced by at least 1-2 points according to the overall Ishak score in
CC the HCV-infected mammal. Also included are a method for predicting
CC changes in liver disease in a chronic HCV-infected mammal, a therapeutic
CC HCV vaccine composition (comprising at least one purified or a
CC combination of at least 2 HCV single or specific oligomeric recombinant
CC envelope protein selected from an E1 or E2 protein, a part of E1 and E2
CC proteins, an E1/E2 protein complex formed from purified HCV single or
CC specific oligomeric recombinant E1 or E2 proteins or its parts and
CC optionally a pharmaceutical adjuvant), a composition (comprising at least
CC one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an
CC immunogenic HCV composition (or HCV vaccine composition) comprising a
CC recombinant virus allowing expression of at least one HCV recombinant
CC envelope protein (selected from an E1 protein and/or an E2 protein, and
CC their parts, and optionally, a pharmaceutical adjuvant) and an HCV
CC vaccine composition (comprising a recombinant virus allowing expression
CC of at least one HCV recombinant envelope protein chosen from an E1
CC protein and/or an E2 protein, and parts of the E1 and E2 proteins and,
CC optionally, a pharmaceutical adjuvant. The HCV vaccine composition is
CC useful for reducing liver disease (such as liver fibrosis or its
CC progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in
CC the liver in a chronic HCV-infected mammal, or for treating a chronic HCV
CC -infected mammal, particularly human. The HCV E1 proteins are useful for
CC in vitro monitoring HCV disease or prognosing the response to treatment
CC of patients suffering from HCV infection. The present sequence is an HCV
CC cDNA encoding an E1 protein (or fragment).


```
PN JP04349885-A.
XX
PD 04-DEC-1992.
XX
PF 29-MAY-1991; 91JP-00152169.
XX
PR 29-MAY-1991; 91JP-00152169.
XX
PA (TEIJ ) TEIJIN LTD.
XX
XX WPI; 1993-022708/03.
XX
XX Envelope region nucleic acid fragment - for type C hepatitis virus (I),
PT for producing vaccine.
XX
XX Claim 1; Page 2; 13pp; Japanese.
XX
CC This sequence encodes a novel envelope region of type C hepatitis virus
CC (HCV). This fragment can be used for the preparation of a vaccine for
CC hepatitis C. This fragment was prepared from the serum of non-A, non-B
CC hepatitis patients and the envelope region DNA was amplified by PCR using
CC the primer sequences given in AAQ35073-76
XX
SQ Sequence 565 BP; 61 A; 92 C; 106 G; 85 T; 0 U; 221 Other;

Query Match 49.1%; Score 219.4; DB 2; Length 565;
Best Local Similarity 45.2%; Pred. NO. 2.5e-58;
Matches 202; Conservative 143; Mismatches 102; Indels 0; Gaps 0;

QY 1 GACGGAAATTAATTTCGACACAGGGAATTTACCTGGTTGCTCTTCTCTATCTTCTCTCTG 60
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 34 GACRGGGTGACTAYGACACAGGGAAYTDCYGGTTCYCTTCTATCTCTCTCTCTCTT 93
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Db 94 GCYTBCTVCTGYTGTACRYBCHGYVTCRCYAVVARGTCRCACAGSSWCMGGG 153
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
QY 121 CTCACATGTTACTAAGTACGAGTACGGTAGTATCGTGTATGAGCCGGGATATT 180
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 154 NYRTAYCATGTACBARYGAYTGYYCYAACKRAGYATWGTGYAYRARGYRRMGGA 213
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
QY 181 ATCTCCACTTACTCGCTGTGCTCCCTGCTACGCTCTGGCAATACATCAAGATGCTG 240
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 214 ATCMTCGWYDYCCBGGGTGYRYBCCTGYTGYCGSARRRYRRYNNYTCBMGNTGTG 273
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
QY 241 ATCCCTGTGAGCCCYACCGTGCCTGGAAGTCCCTGCGCGCCACCGCTCTCTCCGC 300
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 274 GYRGCGCTBACYCCACGCTGYCYRAGRRAYBVAVVYVCCRCBRYGVNMTWCB 333
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
QY 301 ACCGAGTGGATATGATGGTGGGCGGCCACCCCTATGCTCAGTCTCTACGTAGAGAC 360
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 334 CGBCAVRTCGAYTGTCTYTHGGGRSVGCYRYCTCTGYTCSGCVYTSTAYTGKGRGAY 393
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
QY 361 CTTTGTGGAGCGCTATTCTTGTGGGCGAGGGTCTCTCATGGAGACATGCCAGATTGG 420
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 394 YBTGGCGGTCYGTYYTCTYRYTCYABYGTGTTTACCCTCTMBMCMGSMGDAYGDG 453
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
QY 421 ACTGTCCAGACTGCAACTGTTCCATC 447
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 454 ARDYRCARGRTGYAAATGYTCDMTY 480
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Search completed: March 4, 2005, 11:51:17
Job time : 1060 secs

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Result No.	Query			ID	Description
	Score	Match	Length		
C	1	44.8	10.0	1	AV755731 AV755731
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	3	42.6	9.5	1517	BE636546 rockeffell
	4	42.6	9.5	1559	BE636668 rockeffell
	5	39.6	8.6	1561	BE636534 rockeffell
	6	38.6	8.6	562	BM321463 rockeffell
	7	38.6	8.6	270	BE636547 rockeffell
	8	38.6	8.6	409	BE636640 rockeffell
	9	38.6	8.6	482	BM320876 rockeffell
C	10	38.6	8.6	571	BE636646 rockeffell
	11	38.6	8.6	650	BM321414 rockeffell
	12	38.6	8.6	1416	CL961612 OsIFCC006
	13	37.4	8.4	1538	BE636716 rockeffell
	14	37.2	8.3	924	BO707541 AGENCOURT
	15	37.2	8.3	458	H29400 ym60b07_r1
	16	37.2	8.3	555	BM490244
	17	37	8.3	876	BF339031 602034820
	18	36.8	8.2	643	BM321147 rockeffell
C	19	36.8	8.2	561	BE726729 894093B12
	20	36.8	8.2	581	BE452448 894064E06
	21	36.8	8.2	631	BO763234 EBR002 SQ
	22	36.8	8.2	642	BU652417 1112095H0
	23	36.8	8.2	679	CF134176 WHE4368_G
	24	36.8	8.2	688	BE519519 HV_CEB001
	25	36.8	8.2	799	BF621718 HV5N6A001
	26	36.8	8.2	688	BE519519 HV_CEB001
	27	36.8	8.2	688	BE519519 HV_CEB001

Dbb 473 GGTGGTGCACACTCGCTCTG

	Query Match	10.0%;	Score 44.8;	DB 1;	Length 488;
	Best Local Similarity	63.8%;	Pred. No. 0.061;		
	Matches	83;	Conservative	1;	Mismatches 43; Indels 3; Gaps 1;
QY	318	GGTGGGRCGGCCAC	CCTATGCTCAGCTCT	CTACGTAGGAGACCTTTGTGGACGCGTATT	377
Db	473	GGTGGTGCACACT	CGCTCTGTGCTCAGCTCT	CTACGTGTGGACCTCTGGACCGGAGTGAT	414

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QY 378 TCTTGYGGCAGGGTTCTCATGGAGACATCCGACGATTTGGACTGTCTCAGGACTGCAA 437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 413 GCTTGCAGTTTCAGTGATCATCTGG---CCTCAGCACCATGAGTTTGTGATGAATGCAA 357
QY 438 CTGTTCATC 447
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 356 CTGCTCATC 347

RESULT 2
BE636546
LOCUS
DEFINITION
rockefeller.0.126 Mastigamoeba balamuthi lambda ZAP II Library
Mastigamoeba balamuthi cDNA similar to elongation factor 1 alpha,
mRNA sequence.
ACCESSION
BE636546
VERSION
1
KEYWORDS
SOURCE
ORGANISM
Mastigamoeba balamuthi
Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
REFERENCE
1 (bases 1 to 1517)
AUTHORS
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
TITLE
The analysis of 100 genes supports the grouping of three highly
divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
MEDLINE
21819461
PUBMED
11830664
COMMENT
On Aug 25, 2000 this sequence version replaced gi:9919657.
Contact: Muller Miklos
Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
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QY 302 CGCAGTGTGATGATGTGGGGCGGACCGCTATGCTCAGCTCTTACGTAGGAGACC 361
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Db 1425 GTGACTGCCCTAT 1439

RESULT 3
BE636668
LOCUS
DEFINITION
rockefeller.0.341 Mastigamoeba balamuthi lambda ZAP II Library
Mastigamoeba balamuthi cDNA similar to elongation factor 1 alpha,
mRNA sequence.
ACCESSION
BE636668
VERSION
2
KEYWORDS
SOURCE
ORGANISM
Mastigamoeba balamuthi
Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
REFERENCE
1 (bases 1 to 1559)
AUTHORS
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
TITLE
The analysis of 100 genes supports the grouping of three highly
divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
MEDLINE
21819461
PUBMED
11830664
COMMENT
On Aug 25, 2000 this sequence version replaced gi:9919779.
Contact: Muller Miklos
Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
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Matches 99; Conservative 1; Mismatches 95; Indels 0; Gaps 0;
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RESULT 4
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DEFINITION
rockefeller.0.102 Mastigamoeba balamuthi lambda ZAP II Library
Mastigamoeba balamuthi cDNA similar to elongation factor 1 alpha,
mRNA sequence.
ACCESSION
BE636534
VERSION
2
KEYWORDS
SOURCE
ORGANISM
Mastigamoeba balamuthi
Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
REFERENCE
1 (bases 1 to 1561)
AUTHORS
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.

```

TITLE The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)

MEDLINE 21819461

PUBMED 11830664

COMMENT On Aug 25, 2000 this sequence version replaced gi:9919645.

Location/Qualifiers

1. .1561

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/mol_type="mRNA"

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/db_xref="taxon:108607"

/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"

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ORIGIN

Query Match 9.5%; Score 42.6; DB 2; Length 1561;

Best Local Similarity 50.8%; Pred. No. 0.33; Mismatches 95; Indels 0; Gaps 0;

Matches 99; Conservative 1;

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DB 1321 TCGGTGTATCAAGACCGTCTGCGCAAGGTCCCGCGCAAGACCGTGGCGCGCGGACA 1380

QY 302 CGCAGCTGATATGATGTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAGGAGACC 361

DB 1381 AGAGGAGCCCAAGAGAAGTGAAGCGCTCTGCTGCTGCAACCTCTCTAAGAGAGC 1440

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DB 1441 GTGGACTGGCCCTAT 1455

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LOCUS BM321463.1 GI:18055869

DEFINITION Mastigamoeba balamuthi lambda ZAP II Library

Accession BM321463

Version BM321463.1

Keywords EST.

Source Mastigamoeba balamuthi

Organism Mastigamoeba balamuthi

Reference Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.

Authors Baptiste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.

Title The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba

Journal Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)

Medline 21819461

Pubmed 11830664

Comment Contact: Muller Miklos

Location/Qualifiers

1. .1561

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/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"

/note="syn: Phreatamoeba balamuthi"

ORIGIN

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Best Local Similarity 50.8%; Pred. No. 0.33; Mismatches 95; Indels 0; Gaps 0;

Matches 99; Conservative 1;

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QY 302 CGCAGCTGATATGATGTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAGGAGACC 361

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BM321463

LOCUS BM321463.1 GI:18055869

DEFINITION Mastigamoeba balamuthi lambda ZAP II Library

Accession BM321463

Version BM321463.1

Keywords EST.

Source Mastigamoeba balamuthi

Organism Mastigamoeba balamuthi

Reference Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.

Authors Baptiste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.

Title The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba

Journal Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)

Medline 21819461

Pubmed 11830664

Comment Contact: Muller Miklos

Location/Qualifiers

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DB 352 TCGGTGTATCAAGACCGTCTGCGCAAGGTCCCGCGCAAGACCGTGGCGCGCGGACA 411

QY 302 CGCAGCTGATATGATGTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAGGAGACC 361

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RESULT 6

BE36547

LOCUS BE36547.1 GI:9919658

DEFINITION Mastigamoeba balamuthi lambda ZAP II Library

Accession BE36547

Version BE36547.1

Keywords EST.

Source Mastigamoeba balamuthi

Organism Mastigamoeba balamuthi

Reference Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.

Authors Baptiste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.

Title The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba

Journal Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)

Medline 21819461

Pubmed 11830664

Comment Contact: Muller Miklos

Location/Qualifiers

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Db 28 TCGGTGTATCAAGACCGTCTGCGCAAGGTCCCGGCAAGACCGGTGCGCGCGGCA 87
 QY 302 CCACGTGTATGATGTCGGCGCGCCACCTATGCTCAGCTCTCTACGTAGGAGAC 361
 Db 88 AGAAGGACGCCAAGAAGTGAGCAGCGCTCTTGTCTGCAACCTCTTAAGAGAGC 147
 QY 362 TTTGTGGAGCGCTAT 376
 Db 148 GTGGACTGGCCCTAT 162

RESULT 7
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 DEFINITION Mastigamoeba balamuthi linear EST 03-JAN-2002
 rockefeller.0.284 Mastigamoeba balamuthi lambda ZAP II Library
 Mastigamoeba balamuthi cDNA similar to elongation factor 1 alpha,
 mRNA sequence.

ACCESSION BE636640
 VERSION BE636640.1 GI:9919751
 KEYWORDS EST.

SOURCE Mastigamoeba balamuthi
 ORGANISM Mastigamoeba balamuthi

REFERENCE 1 (bases 1 to 409)
 Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.

AUTHORS Baptiste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
 Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
 Philippe,H.

TITLE The analysis of 100 genes supports the grouping of three highly
 divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
 MEDLINE 21819461
 PUBMED 11830664

COMMENT Contact: Muller Miklos
 Laboratory of Biochemical Parasitology
 The Rockefeller University
 1230 York Avenue, New York, NY 10021, USA
 Email: mmuller@rockvax.rockefeller.edu
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 QY 362 TTTGTGGAGCGCTAT 376
 Db 272 GTGGACTGGCCCTAT 286

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 Mastigamoeba balamuthi cDNA similar to elongation factor 1 alpha,
 mRNA sequence.

ACCESSION BM320876
 VERSION BM320876.1 GI:18055282
 KEYWORDS EST.
 SOURCE Mastigamoeba balamuthi
 ORGANISM Mastigamoeba balamuthi

REFERENCE 1 (bases 1 to 482)
 Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.

AUTHORS Baptiste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
 Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
 Philippe,H.

TITLE The analysis of 100 genes supports the grouping of three highly
 divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
 MEDLINE 21819461
 PUBMED 11830664

COMMENT Contact: Muller Miklos
 Laboratory of Biochemical Parasitology
 The Rockefeller University
 1230 York Avenue, New York, NY 10021, USA
 Email: mmuller@rockvax.rockefeller.edu
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FEATURES Location/Qualifiers

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RESULT 9
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 LOCUS BE636646.1 GI:9919757

DEFINITION Mastigamoeba balamuthi linear EST 03-JAN-2002
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 mRNA sequence.

ACCESSION BE636646
 VERSION BE636646.1 GI:9919757
 KEYWORDS EST.

SOURCE Mastigamoeba balamuthi
 ORGANISM Mastigamoeba balamuthi

REFERENCE 1 (bases 1 to 571)
 Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.

AUTHORS Baptiste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
 Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
 Philippe,H.

TITLE The analysis of 100 genes supports the grouping of three highly
 divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
 MEDLINE 21819461
 PUBMED 11830664

COMMENT Contact: Muller Miklos
 Laboratory of Biochemical Parasitology
 The Rockefeller University

1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
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FEATURES

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QY 302 CGCAGCTGGATATGATGTGGGCGGCCACCCCTATGCTCAGCTCTCTACGTAGGAGACC 361
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Db GTGGACTGGCCCTAT 452

RESULT 10

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LOCUS rockefeller.0.1246 Mastigamoeba balamuthi lambda ZAP II Library
DEFINITION Mastigamoeba balamuthi cDNA similar to elongation factor 1 alpha,
mRNA sequence.

ACCESSION BM321414
VERSION BM321414.1 GI:18055820
KEYWORDS EST.

SOURCE Mastigamoeba balamuthi
ORGANISM Mastigamoeba balamuthi

REFERENCE 1 (bases 1 to 650)
AUTHORS Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sengen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
Philippe, H.

TITLE The analysis of 100 genes supports the grouping of three highly
divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
MEDLINE 21819461
PubMed 11830664

COMMENT Contact: Muller Miklos
Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
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FEATURES

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/note="syn: Phreatamoeba balamuthi"

ORIGIN

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Matches 74; Conservative 1; Mismatches 60; Indels 0; Gaps 0;

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Db AGAAGGACGCCCAAGAAGTGAAGTGAAGTCCCGGCAAGACCGGTGCGCGCGCGCA 529
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RESULT 11

CL961612
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

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Db ATACCGCGGAGGCCCAACTCCGACGTGTGGCGCGCGCGCGCGCGCGCGCGCGCG 786

QY 301 ACGCAGCTGGATATGATGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 331
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RESULT 12

BE636716
LOCUS

DEFINITION

rockefeller.0.427 Mastigamoeba balamuthi lambda ZAP II Library
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linear EST 03-JAN-2002
mRNA
rockefeller.0.427 Mastigamoeba balamuthi lambda ZAP II Library
Mastigamoeba balamuthi cDNA similar to elongation factor 1 alpha,

mRNA sequence.
 BB636716
 VERSION BB636716.1 GI:9919827
 KEYWORDS EST.
 SOURCE Mastigamoeba balamuthi
 ORGANISM Mastigamoeba balamuthi
 Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
 1 (bases 1 to 1538)
 Baptiste, E., Brinkmann, H., Lee, J. A., Moore, D. V., Senses, C. W.,
 Gordon, P., Durifle, L., Gaasterland, T., Lopez, P., Muller, M. and
 Philippe, H.
 The analysis of 100 genes supports the grouping of three highly
 divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba
 Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
 21819461
 11830664
 Contact: Muller Miklos
 Laboratory of Biochemical Parasitology
 The Rockefeller University
 1230 York Avenue, New York, NY 10021, USA
 Email: mmuller@rockefeller.edu
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 Best Local Similarity 54.8%; Pred. No. 4.9;
 Matches 74; Conservative 1; Mismatches 60; Indels 0; Gaps 0;
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 QY 302 CCACGTGTGATATGTTGGGCGCGCCACCCATATGCTCAGCTCTCTACGTAGAGACC 361
 DB 1385 AGAAGACGCCAAGAAGTGAAGCGCGCTCTGTCTGTGCAACCTCTCTAAGAGAGC 1444
 QY 362 TTGTGGAGCGCTAT 376
 DB 1445 GTGGACTGCGCTAT 1459
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 LOCUS BQ707541.1
 DEFINITION AGENCOURT_7983174 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215507
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 VERSION BQ707541.1 GI:21846440
 KEYWORDS EST.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 924)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail@nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM2384 row: i column: 12
 High quality sequence stop: 644.
 Location/Qualifiers
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FEATURES

source

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 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 8.4%; Score 37.4; DB 5; Length 924;
 Best Local Similarity 64.4%; Pred. No. 10;
 Matches 56; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 QY 27 TTTACCTGGTTGCTCTTCTCTATCTTCCTTCGCTTCTCATGCTTGTCTTACAC 86
 DB 191 TTTTGTGTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 132
 QY 87 CACAGCCGGCTGGAGTACCGTAATGC 113
 DB 131 GTCACCCAGGCTGGAGTGCAGTGTGC 105
 RESULT 14
 H29400
 LOCUS H29400.1
 DEFINITION Ym60b07.r1 Soares infant brain INIB Homo sapiens cDNA clone
 IMAGE:52725 5', mRNA sequence.
 ACCESSION H29400
 VERSION H29400.1 GI:900310
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 458)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 1974
 High quality sequence stops: 319 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
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source

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